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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	RESULT 1 108277 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		44 44 45	41 42																					200 5 1	(00/03		Result No. S
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n. iffied. ses 1 to 459) A.E. pastoris glyceraldehyde-3-phosphate ED 0374913-Al 2 27-JUN-1990; Location/Qualifiers	459 bp DNA nt EP 0374913.	ALIGNMENTS	CJU76923 SOU76922 HSU25677	HUMLSZA	GGU76913	BC004147	E01888	HUMLSZH	PPU76914	დგ	CTU76920	BOVLYSOZYM	PELYSOC	TOU76917 TFU76918	BOVLSZUA	BOYLZYM14D	AXILZMI	SHPLZM4A SHPLZM4B	SHPLZM1A	SHPLZM1C	SHPLZM3A SHPLZM1B	BOVLSZIA BOVLSZIC	BOVLSZ1B	BOVISZ3A	BOVLSZ2A	BOVLZYM7A	IO8277 BOVLSZ2B	ID
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Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                         Mammalia; Eutheria; Cetart
Bovidae; Bovinae; Bos.
1 (bases 1 to 951)
Irwin, D.M. and Wilson, A.C.
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                 /protein_id="AAA30629.1"
/db_xref="GI:163317"
                                              /codon_start
                                                       /note="lysozyme 2b precursor"
                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
translation="MKALVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA"
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                                                                                                                               Multiple cDNA sequences of bovine tracheal lysozyme J. Biol. Chem. 268 (36), 27440-27446 (1993) 94086565
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                                                                                                                                                                                                                                                                                                    Bos taurus lysozyme
L23758
L23758.1 GI:387905
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   b
            /organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="epithelial/ gland"
/tissue_type="trachea"
/dev_stage="adult"
                                                                                                 Location/Qualifiers
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Sequence 1 from patent US 5422108,
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MIrkov,T.Erik. and Fitzmaurice,L.C.
Protection of plants against plant pathogens
Patent: US 5422108-A 1 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                  Unknown
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                                              GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
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Bovine lysozyme c isozyme 2a mRNA, complete cds.
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Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable sequence by D.M.Irwin, 23-JUN-1989.
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                 GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                            GGCTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
Biol. Chem. 264 (19), 11387-11393 (1989)
                                                                                                                                                                                     282
                                                                                                          Conservative
                                                                                                                                                                                                                /note="lysozyme 2a signal peptide" 50. 436
                                                                                                                                                                                   /product="lysozyme
154 c 187 g
                                                                                                                                                                                                                                                           /codon_start=2
/protein_id="AAA30628.1"
/protein_id="AAA30628.1"
/db_xref="GI:163315"
/translation="TLVILGFLFLSVAVQGKVFERCELARTIKKLGLDGYKGVSLANW
/translation="TLVILGFLFLSVAVQGKVFERCELARTIKKLGLDGYKGVSLANW
LCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELME
NDIAKAYACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                                                                                                     /note="lysozyme 2a precursor"
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/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 963)
Digan, M.E., Harpold,M.M., Lair,S.V., Thill,G.P., Siegel,R.S.,
Ellis,S.B. and Williams,M.E.
PRODUCTION OF ANIMAL LYSOZYME c VIA SECRETION FROM PICHIA PASTORIS
AND COMPOSITION THEREFOR
PATENT: WO 8904320-A 1 18-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1 from Patent WO 109315 109315.1 GI:587976
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
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  CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                                                                                                                                     GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                       GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                           GTGTAATGATGCCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
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165 c 200 g
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O 8904320.
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TITLE
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Best Local Similarity
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Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lysozyme
           ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                             GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                               TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                              ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                  TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGATGGCTATAAGGGA 128
ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 188
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                                                                                                                                                                                                                                                                     343
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                           /protein_id="AAA30632.1"
/db_xref="GI:163333"
/db_xref="GI:16333"
/translation="MRALIILGELFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA
.NWLCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
.MENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVQGCTL"
                                                                                                                                                                                                                                                                                           /note="lysozyme 3a signal peptide" 63. .449
                                                                                                                                                                                                                                                                 /product="lysozyme 3a"
205 c 209 a
                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                       /note="lysozyme 3a precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
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                                                                                                                                                                                                                96.0%;
97.5%;
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DB 4;

Length 1082; Indels

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J. Biol. Chem. 264 (19), 11387-11393 (1989)
89291894
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BOVLS23A 1082 bp
Bovine lysozyme c isozyme 3a mRNA,
M26242 J04831 M27180
M26242 1 GI:163322
Draft entry and computer-readable sequence by D.M.Irwin, 23-JUN-1989.
                                                                                                                      Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                                                                                                              Bovine abomasum, cDNA to mRNA, clone lambda-cBL[26,28].
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                   [1] kindly submitted
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Matches 429
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128
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Bovine lysozyme c isozyme 1b mRNA, complete cds.
M26246 J04831 M27179
M26246.1 GI:163312
                                                                                                            8
                                                                                                                                       1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Draft entry and computer-readable by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multiple cDNA sequences and the evolution of bovine stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 891)
Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine abomasum, cDNA to mRNA, clones lambda-cBL[3,4,35].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                                                      TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
GTCAGTCTGGCAAACTGGCTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 187
                                                       TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGATGGCTATAAGGGA
                                                                                                            ATGAAGGCTCTCATTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                          274
                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                        /product="lysozyme 1b"
152 c 196 g
                                                                                                                                                                                                                                                                                                           /translation="mkallilgflflsvavqgkvfercelartlkklgldgykgvsla
NWLCLTKWESSYNTKATNYNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
MENELAKAVACAKQIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAA30627.1"
/db_xref="GI:163313"
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                  /note="lysozyme 1b signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                /note="lysozyme 1b precursor"
                                                                                                                                                                                                                                                                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                      .448
                                                                                                                                                                                 94.6%;
                                                                                                                                                                    Score 420; DB 4;
Pred. No. 6e-105;
0; Mismatches 1
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                                                                                                                                                                                                DB 4; Length 891;
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AUTHORS
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ACCESSION
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                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                        sig_peptide
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                                                                                                               427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine lysozyme c isozyme la mRNA,
M26245 J04831 M27178
M26245.1 GI:163310
                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
1 (bases 1 to 906)
Irwin,D.M. and Wilson,A.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2738070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 264 (19), 11387-11393
89291894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine abomasum, cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOYLSZ1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lysozyme
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGTTGAGGGTTGCACGCTGTAA 451
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                                                                                                                                                                                    276
                                                                                                               Conservative
                                                                                                                                                                                  /product="lysozyme la"
155 c 198 g
                                                                                                                                                                                                                                                                                               /protein_id="AAA30626.1"
/db_xref="GI:163311"
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /codon_start=]
                                                                                                                                                                                                                                                                                                                                         /note="lysozyme la precursor"
                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                     .906
                                                                                                                           93.9%;
                                                                                                               0;
                                                                                                                           Score 416.8; DB 4;
Pred. No. 4.6e-104;
                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906 bp
                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
23 ATGAAGGCTCTCATTATTCTGGGGTTTCTCTTCCTTTCTGTTGCTGTCCAGGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multiple cDNA sequences and the evolution of bovine stomach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTAATGGAAAATGAGATCGCGAAAGCTGTAGCGTGTGCCAAGCAGATTGTCAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGGCATTACAGCATGGGTGGCATGGAAAAGTCACTGTCGAGACCATGACGTCAGCAGT
                                                                                                                       /note="lysozyme la signal peptide"
77. .463
                                                                                                                                                                                                                                                                                                                                                                                                                                            MENETAKAVACAKQIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Translation="MKALIILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA
NWLCLTKWESSYNTKATNYNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone lambda-cBL21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete cds.
                                                                                                                                                                                                                                             Length 906;
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                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1] kindly submitted
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Best Local :
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                                                                                                                                                mat_peptide
                                                                                                                                                                          sig_peptide
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                                                                     Local
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                                46
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                                                                                                                                                                                                                                                                                                                                         Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
1 (bases 1 to 877)
Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine lysozyme c isozyme M26244 J04831 M27183
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                       2738070
                                                                                                                                                                                                                                                                                                                                                                                                                   Multiple cDNA sequences and the evolution of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine abomasum, cDNA to mRNA, clones lambda-cBL[20,36,39].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M26244.1 GI:163318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVLSZ2C
                                                                                                                                                                                                                                                                                                                                                                                                           Lysozyme
                 GTCCAAGGCAAGGTCTTTGAGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTG 105
    GTCAAAGGCAAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGTGGTGTAATGATGGCAAAACCCCCCAACGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                       285
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Chem. 264 (19), 11387-11393 (1989)
                                                                                                                     /product="lysozyme
142 c 181 g
                                                                                                                                                /note="lysozyme 2c signal peptide"
10. .396
                                                                                                                                                                                 /protein_id="AAA30630.1"
/db_xref="G1:163319"
/db_xref="G1:163319"
/translation="VKGKVFERCELARTLKKLGLDGYKGVSLANWLCLTKWESSYNTK
/translation="VKGKVFERCELARTLKKLGLDGYKGVSLANWLCLTKWESSYNTK
ATNYAPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELMENDIAKAVACAKHI
VSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                              /db_xref="taxon:9913"
<1. .399
                                                                                                                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                             /note="lysozyme 2c precursor"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                     organism="Bos taurus"
                                                                    89.5%;
99.7%;
                                                        0,
                                                                   Score 397.4; DB 4; Pred. No. 1e-98;
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              877
e 2c
                                                                                                                                  2c"
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mRNA,
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                                                    Gaps
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AUTHORS
TITLE
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Best Local
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                                                                                                                                                                    mat_peptide
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  \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sheep abomasum, cDNA to mRNA. Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHPLZM3A 875 bp
Sheep lysozyme 3a (lyz3a) mRNA,
M32496 J05279
M32496.1 GI:165971
lysozyme 3a.
                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                 2318875
                                                                                                                                                                                                                                                                                                                                                                                                                             Irwin, D.M. and Wilson, A.C.
278
                                                    Conservative
                                                                                                                  Ø
                                                                                                                                           /product="lysozyme 3a"
1. .17
                                                                                                                             /note="PCR primer"
                                                                                                                                                                                                                                                                         <1. .390
                                                                                                                                                                     1. .387
                                                                                                                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                                 /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                  148 c
                                                               82.8%;
96.4%;
                                                    0;
                                                                                                               189 g
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406 CATGACGTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 CATATTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTAGCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 GACGGCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGT 165
55 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 CATGACGTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 CATATTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Concerted evolution of ruminant stomach lysozymes. Characterization of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
90202968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Caprinae; Ovis.
1 (bases 1 to 875)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable by D.M.Irwin, 01-MAR-1990.
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                                                                                                                                                                                                                                              QGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                                                                                                                                              /protein_id="AAA31561.1"
/db_xref="GI:165972"
/translation="KVFERCELARTLKKLGLDGYKGYSLANWLCLTKWESGYNTKATN
                                                                                                                                                                                                                                                                 YNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSALMENDIEKAVACAKHIVSE
                                                                                                                                                                                                                                                                                                                                                                      /note="lysozyme 3a precursor"
                                                         Score 367.6; DB 4
Pred. No. 1.6e-90;
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1 (bases 1 to 881)
Irwin,D.M. and Wilson,A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
reiol. Chem. 265 (9), 4944-4952 (1990)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.
1 (bases 1 to 881)
                                                                                                                                                                                                                                                                                                                                                                                                          Draft
by D.M
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                AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT
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 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGGAACTCGGACTGGACGGCTAT
                                                                                                                                          285
                                                                                                                                                                                                                                                                                                                                                                                                            entry and computer-readable M.Irwin, 01-MAR-1990.
                                                                                                                                     /note="PCR primer"
145 c 182 g
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/db_xref="GI:165966"
/translation="KVFERCELARTLKELGLDGYKGVSLANWLCLTKWESSYNTKATN
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                                                                                                                                                                                                                                                                                                                                            /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                   /product="lysozyme 1b"
                                                                                                                                                                                                                     QGITAWVAWKSHCRDHDVSSYVEGCSL"
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1 (bases 1 to 881)

1 (bases 1 to 881)

1 (bases 1 to 881)
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                AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT: 1.14
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 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGGAACTCGGACTGGACGGCTAT 60
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                                                                                                                                        /note="PCR primer"
1 144 c 183 g
                                                                                                                                                                      /product="lysozyme lc"
1. .17
                                                                                                                                                                                                     QGITAWVAWKSHCRDHDVSSYVEGCSL"
1. .387
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/taasslatton="Kytercelartilkelgldgykgyslanwicltkwessyntkatn
/taasslatton="Kytercelartilkelgldgykgyslanwicltkwessyntkatn
                                                                                                                                                                                                                                                                                                                                 <1. .390
                                                                                                                                                                                                                                                                                                                                          /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                             /note="lysozyme 1c precursor"
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                                                          Score 367.6; DB 4
Pred. No. 1.6e-90;
0; Mismatches 14
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 881)
1 rwin, D.M. and Wilson, A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lysozyme 2a.
Sheep abomasum, cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHPLZM2A 881 bp
Sheep lysozyme 2a (lyz2a) mRNA,
M32495 J05279
                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable sequence by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M32495.1
 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAAC
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                                                     Conservative
                                                                                                                                                                                                                                                                              /organism="Ovis aries"
/db_xref="taxon:9940"
<1. .390</pre>
                                                                                                                                   /note="PCR primer"
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                                                                                                                                                  /product="lysozyme
1. .17
                                                                                                                                                                                                                                                       /codon_start=
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                  /note="lysozyme 2a precursor"
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                                                                  82.8%;
96.4%;
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                                                     Score 367.6; DB 4;
Pred. No. 1.6e-90;
D; Mismatches 14;
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M32492 J05279
M32492.1 GI:165963
                                                                                                                                                                                                                                                                                                                                                                                            Concerted evolution of ruminant stomach lysozymes. of lysozyme cDNA clones from sheep and deer J. Blol. Chem. 265 (9), 4944-4952 (1990)
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1 (bases 1 to 881)
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            AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT 114
  AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGGAACTCGGACTGGATGGCTAT
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                                                     Conservative
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1. .15
                                                                                                                    /note="PCR primer"
144 c 182 g
                                                                                                                                                                                                                                                                                      /organism="Ovis aries"
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                                                                                                                                                                                                                                                             /note="lysozyme la precursor"
                                                                82.4%;
                                                   0;
                                                                Score 366; DB 4;
Pred. No. 4.5e-90;
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ted: July 5, 2003, 06:13:47 83 secs	Search completed: July Job time : 1383 secs	JC 9S
AGCAGTTATGTGGAGGGTTGCTCCCTGTAA 390	361	밁
AGCAGTTACGTTGAGGGTTGCACCCTGTAA 444	415	γQ
AGTGAGCAAGGCATTACAGCATGGGTGGCTTGGAAAAGTCACTGTCGAGACCATGACGTC 360	301	Ъ
AGTGAGCAAGGCATTACAGCCTGGGTGGCATĞGAAAAGTCATTGTCGAGACCATGACGTC 414	355	Qγ
TGCAGCGAATTAATGGAAAATAACATCGCTAAAGCTGTAGCATGTGCAAAGCATATTGTC 300	241	αa
TGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTC 354	295	Qy
AGCAAGTGGTGTAATGATGGCAAAACCCCTAACGCAGTTGACGGCTGTCATGTGTCC 240	181	ДD
AGCAAATGGTGGTGAATGATGGCAAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCC 294	235	Qy
AAAGCTACAACTACAATCCTGGCAGTGAAAAGCACTGATTATGGGATATTTCAGATCAAC 180	121	ф
AAAGCTACAAACCTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAAC 234	175	Qy
AAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACA 120	61	DЬ
AAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACA 174	115	Qy

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OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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437.4
435.8
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Listing first 45 summaries
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990_DAT:

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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA20010_DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A_DAT:

SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B_DAT:

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Copyright (c) 1993 - 2003 Compugen Ltd.
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Bovine Lysozyme c2
ss sequence of CDN
Bovine lysozyme c
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Human benign prost
Sequence encoding
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coding for the
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Mutant human lysoz	AAQ52670	14	396	35.2	156.2	5
Human colon cancer	ABQ58989	24	706	35.4	157	4
pPLHLY-2 human lys	AAN81735	9	427	35.4	157.2	ū
` ×	AAN92359	10	394	35.4	157.2	2
Sequence of the Ta	AAN81447	9	394	35.4	•	Ë
	AAN81284	9	394	35.4	٠	ö
	AAN81354	9	394	35.4	•	9
of Taq	AAN60214	7	394	•	•	8
Synthetic human ly	AAN70537	œ	418		٠	37
Sequence encoding	AAN60953	7	418		•	8
Human lysozyme. H	AAQ52669	14	396		•	5
Human lysozyme gen	AAQ06558	11	396			34
Sequence of natura	AAN90966	10	396		•	ü
Human lung tumour	ABK16005	24	233		•	ະ
Sequence of synthe	AAN60206	7	390	٠		<u>~</u>
Human lysozyme cod	AAI64878	22	390		169.6	ö
Mutant human lysoz	AAQ03795	H	399		175.4	9
Avian lysozyme sig	AAQ13590	12	444		176.2	8
Human lysozyme DNA	AAN90102	10	447		176.6	27
Synthetic human ly	AAQ10356	12	464		185.4	8
Human colon tumour	ABL38017	24	585	41.8	185.6	Š
Synthetic human ly	AAQ03794	1	449		187.8	24
Nucleotide sequenc	AAF55437	22	614		222.6	ä
Sequence encoding	AAN70944	8	390	53.8	239	ວ
Human colon cancer	AAA16339	21	657		250	1
DNA encoding novel	AAS66076	23	1798			õ
Human macrophage-e	AAD17740	22	444	•	•	٥
Human lung-specifi	AAD39104	24	2467	59.7	265.2	ω
Human colon tumour	ABL37496	24	481		267.8	7
Sequence encoding	AAN70943	œ	447			9
Sequence of human	AAN92054	10	435		269.2	5
Sequence encoding	AAN70949	æ	490		•	4
Pancreas cancer re	ABL70110	24	748		279	ω
Human prostate exp	ABV24794	23	1776	63.2	280.6	N
DNA encoding novel	658	23	1512	•	280.6	<u>-</u>
Human macrophage-e	AAD17725	22	1512	63.2	280.6	0

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ALIGNMENTS

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RESULT 1
AAD39128
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                                                                                                                                                                                                                                                                                       17-OCT-2001; 2001WO-US32147
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Pogue G,
                                                                                                  (LARG-) LARGE SCALE BIOLOGY CORP
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/product= "Bovine lysozyme'
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RESULT 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to viral vectors and methods for producing transgenic plants that express heterologous DNA that encode a ruminant lysozyme, preferably bovine. This lysozyme protects against diseases caused by plant pathogens particularly bacterial pathogens. The method is useful for producing bovine lysozyme in host plants e.g. grapevines. Plasmid encoding a recombinant plant virus which comprises a bovine lysozyme encoding nucleic acid, is useful for producing bovine lysozyme protech which acts as an anti-Xylella reagent for development of a recombinant source of BoLys protein for treating grapevines against Pierce's disease (PD). The method is useful for protecting grapevines against Xylella fastidiosa bacterium infection that causes PD. The present sequence is bovine lysozyme DNA.
               Sequence encoding bovine lysosyme
                                              30-OCT-1990
                                                                                                              AAQ05054 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 444 BP; 128 A; 86 C; 117 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful for protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys
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                                              (first entry)
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Best Local :
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the cell to produce bovine lysosyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 459 BP; 132 A; 89 C; 119 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence may be inserted into the DNA of Pichia pastoris at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel DNA fragments comprising Pishia pastoris GAPDH gene it's 5'-regulatory region and 3'-transcription termination
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additive homogenous recombination; bovine lysosyme c2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
            TACGTTGAGGGTTGCACCCTGTAA 444
                                                                CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACCATCAGCAGT
                                                                                                                                                                        TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGCAAAGCATATTGTCAGTGAG
TACGTTGAGGGTTGCACCCTGTAA 450
                                                   CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                       GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                             ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                                                                                                                                                 TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disrupting the gene activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Pred. No. 3.4e-127;
Mismatches 0;
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RESULT 3
AAD39129
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AAD39129 standard; DNA; 10130 BP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovine; viral vector; transgenic plant; lysozyme; antibacterial; Pierce's disease; PD; Xylella fastidiosa bacterium infection; anti-Xylella reagent; grapevine; cyclic; circular; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovine; viral vector; Pierce's disease; PD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p1044-BoLys plasmid DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 2; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2000; 2000US-240967P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200233041-A2
                                                                                                                                                                                                                                                                                                                      Sequence 10130 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2001; 2001WO-US32147
                                                                                                                                                                                                                                                                                                                                                                    present sequence is p1044-BoLys plasmid DNA containing bovine lysozyme
                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                          5767
                                                                                                                          5827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-479667/51.
                              181
                                                                                            121
                                                                                                                                                                                                                                                        444;
                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LARGE SCALE BIOLOGY CORP
                                                         TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                          ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTCTGTCGCTGTCCAAGGCAAGGTC
ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
               ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                          TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                                                          ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Velichko S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 5767..6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "Bovine lysozyme
                                                                                                                                                                                                                                                                                                               2854 A; 2078 C; 2492 G; 2706 T; 0 other;
                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                     Score 444; DB 24;
Pred. No. 1.2e-126
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA"
                                                                                                                                                                                                                                                                                      Length 10130;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                      Gaps
                            . 240
                                                                                                                                                          120
                                                            5946
                                                                                                                                                                                                                          60
9006
                                                                                                                          5886
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RESULT 4
AAV08922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                used in the transgenic plant of the invention. The transgenic plant is resistant to plant pathogens and contains heterologous DNA encoding a ruminant or ruminant-like lysozyme, the plant expresses sufficient levels of the lysozyme to render it less susceptible to the pathogens than the wild type plant. The plants are resistant to bacterial pathogens such as
                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine Lysozyme c2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV08922 standard;
                                                                                                This sequence encodes the bovine lysozyme c2 and can be
                                                                                                                        Example 1; Column 37-40; 23pp; English.
                                                                                                                                                         Transgenic plants resistant to bacterial pathogens - contain
                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                      Fitzmaurice LC,
                                                                                                                                                                                                                                                                                   19-SEP-1991;
25-NOV-1991;
                                                                                                                                                                                                                                                                                                                                   22-APR-1997;
                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                  US5850025-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogen resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lysozyme; signal peptide; transgenic plant; plant pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV08922;
                     Pseudomonas syringae or Erwinia carotovora.
                                                                                                                                              ruminant lysozyme
                                                                                                                                                                                                                                              (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                                                                                                                                                                                                                                         12-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6187
                                                                                                                                                                                             1999-069855/06
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                                                                                                                                                                                    AAW73502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACGTTGAGGGTTGCACCCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGTTGAGGGTTGCACCCTGTAA 6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                      91US-0762679.
91US-0798223.
97US-0919093.
                                                                                                                                                                                                                                                                                                          95US-0373390
                                                                                                                                                                                                                                                                                                                                   97US-0919093
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
25..462
/*tag= a
                                                                                                                                                                                                                       Mirkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6186
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Matches 439; Query Match Best Local

Similarity

100.0%; 98.98;

Score 439; DB 20; ; Pred. No. 1.6e-125;

Length 964; Indels

0; Gaps

0

Conservative

0;

Mismatches

Sequence 964 BP; 297 A; 165 C; 201 G; 301 T; 0 other;

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RESULT 5
AAN92057
ID AAN9
XX AAN9
XX AAN9
XX BOV1
XX B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Б
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       (SALK ) SALK
                                        02-NOV-1987;
                                                                        02-NOV-1988;
                                                                                                           18-MAY-1989
                                                                                                                                                                                              3'UTR
                                                                                                                                                                                                                           mat_peptide
                                                                                                                                           WO8904320-A
                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovine lysozyme C2; protein signal sequence; Pinchia pastoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lysozyme C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN92057 standard; DNA; 964 BP
                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN92057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTCTCGTTATICTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAGGGTTGCACCCTGTAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTAATGATGCCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of cDNA insert of clone lambda BL3 encoding bovine together with 3' untranslated region.
       INST FOR BIOL STUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                        87US-0115940.
                                                                        88WO-U503907
                                                                                                                                                                                                         /*tag= c
68..462
/*tag= d
                                                                                                                                                                                           /*tag= 0
                                                                                                                                                                                                                                                                                                          /standard_name=
942..964
                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                              /standard_name=
25..462
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                               /*tag= a
                                                                                                                                                                                                                                                                                                                               "ECORI
                                                                                                                                                                                                                                                                                                                             Adaptor"
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RESULT 6
AAQ39092
ID AAQ3
XX
AC AAQ3
XX
DT 20-J
XX
DE BOV1
XX
KW BOV1
KW Gram
KW Toma
KW Agro
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
              Bovine: lysozyme c; transgenic; plant; resistance; pathogen; gram negative; bacteria; hen egg white lysozyme; potato; tobacc tomato; carrot; apple; sunflower; petunia; violet; Pseudomonas; Agrobacterium; Xanthomonas; Erwinia; Clavibacter; ss.
                                                                                                  Bovine lysozyme c DNA.
                                                                                                                                      20-JUL-1993
                                                                                                                                                                      AAQ39092;
                                                                                                                                                                                                     AAQ39092 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino-terminus of the mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Digan ME, H
Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pages 26-29; ; 85pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1989-165613/22.
                                                                                                                                                                                                                                                                                          444
                                                                                                                                                                                                                                                                                                                                                            384
                                                                                                                                                                                                                                                                                                                                                                                                                             324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
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                                                                                                                                                                                                                                                                                       TGAGGGTTGCACCCTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harpold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                    (first entry)
                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                       964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lair
                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                        462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GP,
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tobacco;

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The 3'-noncoding sequence does not contain a polyadenylation signal or a poly (A)+ tail. The 5'-terminus does not contain the ATG triplet corresponding to the translation initiation codon fo the pre-lysozyme C2 mRNA. Thus the CDNA insert encodes 16 amino acids amino-terminal to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 964 BP; 298 A; 165 C; 200 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of animal lysozyme C from pichia pastoris by secretion consists of P. pastoris promoter and terminator DNA
                       CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT 425
                                                                                                                                                                                                                                                                                                                                                                                                 CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                            AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                                                             GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                  GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                 AATGGAAAATGACATCGCTAAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                                   GTGTAATGATGCCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                       CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 437.4; DB 10;
Pred. No. 5e-125;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ellis SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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443
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the production of transgenic plants that are resistant to pathogens. The lysozyme encoded by this sequence has a greater ability to lyse gram negative bacteria than hen egg white lysozyme and also has a greater stability. The lysozyme may be applied directly to treat or protect plants such as potatoes, tobacco; tomatos, carrots, apples, sunflowers, petunias and violets from plant pathogens such as Pseudomonas, Agrobacterium, Xanthomonas, Erwinia and Clavibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection of plants against plant pathogens - by transforma with DNA encoding a ruminant or ruminant like lysozyme, esp-bovine lysozyme C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 73-74; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes bovine lysozyme c \cdot ^{	ext{	iny This}} This sequence was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-117142/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMAR-) SMART PLANTS INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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426
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                                                                                                                                                                                                                                                                                               126
                                                                                                                                               264
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                                                                                                                                                                                                                                                                                                                                                                                    24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                           GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT 305
                                                                                                                                                                                                        CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                     CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                                  CGTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                                                                              CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                           GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTTGGACTGGACGGCTATAAGCGAGTCAG
                                                                                                                                                                                                                                                                                                                                          GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                  GGCTCTCGTTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    964 BP;
TGAGGGTTGCACCCTGTAA 444
                                                       CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT 425
                                                                                                                 AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAAGG 365
                                                                                                                                             GTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0762679.
91US-0798223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92WO-US07960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 25..459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 A; 165 C; 201 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mirkov TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 435.8; DB 14
Pred. No. 1 6e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 14; Length 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 7
ABK64517
ID ABK64517
ABK64517
ABK64517
AXX ABK6
AXX ABK(
AXX ABK(
AXX Hum)
XXX Hum)
XXX Hom
XX Hom
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2000;
05-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2001; 2001WO-US24708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200212440-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK64517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK64517 standard; DNA; 1483 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 241; 444pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Munger WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; benign prostatic hyperplasia; BPH; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENE LOGIC INC.
(NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-257476/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   444 TGAGGGTTGCACCCTGTAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          benign prostatic hyperplasia gene #412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kulkarni P, Getzenberg RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-223323P
2001US-0873319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene;
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The invention relates to a method of diagnosing (I) the onset or correct progression of benign prostatic hyperplasia (BPH), or screening (II) for corridentifying an agent that modulates the onset or progression of BPH.

CC The method is based on changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate compared to normal prostate tissue. (I) comprises the properties of one or more genes in prostate cells (II) comprises preparing a first gene expression profile correction the subject that are differentially regulated compared to normal corrections the subject that are differentially regulated compared to normal corrections of BPH cells of one or more genes in prostate cells (II) comprises preparing a first gene expression profile correction as econd gene expression profile of the agent exposed (I) is made to proparing the first and second gene expression profiles. (II) is useful for diagnosing the onset or progression of BPH. (II) is correctly in a depart that modulates the onset or progression correctly in a tissue or cells, by comparing the expression correctly in a tissue or cells to the expression level in a tissue or cells, by comparing the expression correctly of genes given in the database, and displaying the compared to the expression level in BPH. Agents using (II) are useful for treating BPH or prostate cancer. ABK64106-ABK64860 represent human contains the prostatic hyperplasia gene sequences of the invention.

Sequence 1483 BP; 432 A; 298 C; 309 G; 444 T; 0 other;

δÃ Matches 1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC Similarity Conservative 63.2%; 78.3%; 0 Score 280.6; DB 24; Pred. Mismatches No. 1.8e-76; smatches 94; Indels Length 1483; ω --

밁 14 ATGAAGGCTCTCATTGTTCTGGGGCTTGTCCTCCTTTCTGTTACGGTCCAGGGCAAGGTC 73

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RESULT 8
AAQ03369
ID AAQ0
AX AAQ0
AX AAQ0
AX Sequ
XX Tran
CX Tran
XX T
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                                                Human lysozyme DNA can be used to obtain transgenic animals, e.g. mice. It can also be produced by culturing animal cells, and it can promote the genetic expression of these animal cells.
Sequence 1494 BP; 441 A; 298 C;
                                                                                                                                                                                                 Human lysozyme gene \cdot useful promoter for genetic expression of animal culturing
                                                                                                                                                                                                                                                                                                        P-PSDB; AAR06108
                                                                                                                                                                                                                                                                                                                                    WPI; 1990-053916/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic animal; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoding human lysozyme
                                                                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEMICAL IND KK
                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP02005879-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ03369 standard; DNA; 1494 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-JAN-1990
                                                                                                                                                         Fig 4-1 to 4-3 Pages 834-835; 13pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 CAGTATGTTCAAGGTTGTGGAGTGTAA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGGTGTAATGATGCCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
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68..460
/*tag= b
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309 G; 446 T; 0 other;
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AAN92386
ID AANS
XX AANS
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DX O3-C
XX DNA
DE (HL)
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COS Home
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Best Local
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                                                 WPI; 1989-127529/17.
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                                                                                                                                                                                                                                                                                                                                                                                                         mat_peptide
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                                                                                                                                             16-SEP-1987;
                                                                                                                                                                                            16-SEP-1987;
                                                                                                                                                                                                                                           20-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAN92386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAN92386 standard; DNA; 1496
                                                                                              (TAKE ) TAKEDA CHEMICAL IND KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 CAGTATGTTCAAGGTTGTGGAGTGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 ATGAAGGCTCTCATTGTTCTGGGGGCTTGTCCTCTTTCTGTTACGGTCCAGGGCCAAGGTC
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68..457
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14..46
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 14..67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signal peptide and mature protein of human lysozyme
                                                                                                                                                                                                                                                                                                                                                          .460
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78.3%;
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Pred. No. 1.8e-76;
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New DNA sequence -

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RESULT 10
AAD17725
ID AAD17725
AC AAD17
XX AD17
XX IO-DE
XX Human
DE Human
XX ITANS
KW Human
KW Trans
KW Gene
KW Gene
KW Sepsi
KW Alzhe
KW Alzhe
KW Throm
KW Throm
KW Unung;
KW Multik
KW Coagu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It is useful for effective expression of human lysozyme in yeast or animal cells. Also, DNA encoding various proteins can be linked to the 3' end of the HL signal peptide so that it is downstream of the promoter of the expression vector. Expression of such proteins is possible in E. coli, Bacillus subtilis, yeast or animal cells. Lysozyme
Human; macrophage-expressed protein; inflammation; angiogenesis; cancer; transplantation; myelodysplastic syndrome; transgenic animal; ischaemia; gene therapy; Crohn's disease; immune disorder; myeloid leukaemia; shock; sepsis; nephritis; genetic disorder; mervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; fibrosis; amyotrophic lateral sclerosis; lymphoid cell disorder; platelet disorder; thrombocytopenia; osteoarthritis; bone degenerative disorder; thrombosis; periodontal disease; osteoprosis; tissue repair; burn; incision; ulcer; multiple sclerosis; rheumatoid arthritis; allergy; asthma; thrombolysis; coagulation disorder; hereditary disorder; haemophilia; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1496 BP; 443 A; 299 C; 308 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding signal peptide and mature protein
                                                                                                                                                                                                                                                                                                                                                                                     AAD17725 standard; cDNA; 1512 BP
                                                                                                                                                                                                                                                      Human macrophage-expressed
                                                                                                                                                                                                                                                                                                  10-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for controlling bacterial infection and unlike chicken lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-1 - 2-1; pages 12-13; 13pp; Japanes
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78.3%;
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Pred. No. 1.
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antidiabetic; antibacterial; immunosuppressive; analgesic; vulnerary; immunostimulant; vaccine; vasotropic; nootropic; haemostatic; osteopathic; fungicide; Location/Qualifiers /*tag= ρ

Homo

mat_peptide sig_peptide /*tag= b 83..472 /product= 29..82 /*tag= C "Human macrophage-expressed protein"

WO200164839-A2

/product=

"Human mature macrophage-expressed protein"

28-FEB-2001; 2001WO-US06475

31-MAR-2000; 11-DEC-2000; 28-FEB-2000; ; 2000US-0515126. ; 2000US-0540217. ; 2000US-0255200.

(HYSE-) HYSEQ INC

Dedera D, L. Boyle BJ, , Jones LW, Labat Liu 'nή Stache-crain Tang YT; В,

P-PSDB; AAE10577 2001-582152/65

Novel macrophage-expressed nucleic acids and polypeptides for diagnosis and treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell disorders, cancer and for promoting wound healing

Claim 1; Page 139-140; 158pp; English

CC differentiation and survival of pluripotent and totipotent stem cells call differentiation and survival of pluripotent and totipotent stem cells cof bio-pharmaceuticals, development of bio-sensors and transplantation. CC The protein is used to manipulate stem cells in culture to give rise to cof bio-pharmaceuticals, development of bio-sensors and transplantation. CC The protein is used to manipulate stem cells in culture to give rise to convice protein is used to manipulate stem cells in culture to give rise to by illness, accidental damage or genetic disorders, induces the clis and is useful for the treatment of central and peripheral nervous system conditions and neuropathies, such as Alzheimer's, Parkinson's disease, conditions and involved in comparative or chemokinetic activity, regulation of haematopolesis and conditions or periodontal disease and for regulation of haematopolesis and conditions or periodontal disease and for regulation of bone, cartilage, conditions or periodontal disease and for regulation of bone, cartilage, conditions or liver fibrosis, immune deficiencies and disorders such as severe combined immunodeficiency (SCID), bacterial or fungal infections, cartilage, considered in thrombolysis or thrombosis is useful in treatment of coagulation and other haemostatic events in treating wounds resulting constrains contacts of the protects of the conditions of the combined in the conditions and the conditions of the combined conditions are such as asthma or other respiratory problems and is involved in thrombolysis or thrombosis is useful in treatment of coagulation or deficiency (SCID) and the combined conditions or the conditions of the conditions of the combined conditions and the conditions of the combined conditions and the conditions of the combined conditions of the combine reperfusion injury, shock, sepsis, immune responses, cancer and myeloid leukaemia and myelodysplastic syndromes. The protein exhibits activity relating to angiogenesis, cytokine, stem cell growth factor activity an transgenic animals. Macrophage-expressed molecule is useful treating inflammatory conditions such as nephritis, Crohn's disease, ischaemia-The present invention relates to an isolated macrophage-expressed cDNA its protein. The invention is used in gene therapy and in creating of male temale subjects

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Best Local
   Drmanac
                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolism, catabolism, anabolism, processing utilisation, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and as an antigen in a vaccine composition to raise an immune response. The present sequence is human macrophage-
                            (HYSE-) HYSEQ INC.
                                                                                                   30-MAR-2001; 2001WO-US08631.
                                                                                                                                 11-OCT-2001
                                                                                                                                                                                                                Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #1685
                                                                                                                                                                                                                                                                                          13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                   AAS65881 standard; cDNA; 1512
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                                                                                                                                                                                                                                                                                                                                                                                                                       449 CAGTATGTTCAAGGTTGTGGAGTGTAA 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTGCTGCAAGATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGTTGTCCGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                         2000US-0540217
2000US-0649167
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78.3%;
Tang YT
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Pred. No. 1.8e
0; Mismatches
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CC Note: The sequence data for this patent did not appear in the printed content of the printed of the printed of the printed of the content of the content of the content of the printed of the content of the content of the printed of the content of the
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1512 BP; 438 A; 308 C; 312 G; 454 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 1685; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTCAGCCTGGCAAACTGGTTTGTGTTTTGACCAAATGGGAAAGCAGTTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTCTTCTGTCGCTGTCCAAGGCAAGGTC
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CAGTATGTTCAAGGTTGTGGAGTGTAA 475
                                      AGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                          GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA- 359
                                                                                                          CACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                  --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC 417
                                                                                                                                                                                                                             GCTTTGCTGCAAGATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGGTTGTCCGTGAT
                                                                                                                                                                                                                                                                                                                                       TACTGGTGTAATGATGGCAAAACCCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGT 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.2%; Score 280.6; DB 2 78.3%; Pred. No. 1.8e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Length
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                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 4747-4748; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV24794 standard; cDNA; 1776 BP
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1776 BP; 523 A; 368 C; 390 G; 492 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 24785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     patient;
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-662795/76.
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                         219
                                                                   121
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                       GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                    TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                     ATGAAGGCTCTCATTGTTCTGGGGGCTTGTCCTCTTTCTGTTACGGTCCAGGGCCAAGGTC
                                                                                                                                                                                                                                               ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                              63.2%;
78.3%;
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                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                            Score 280.6; DB
Pred. No. 2e-76;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                   Length 1776;
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                                                                                                                                                                                                                                                                                         Gaps
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05-JUN-2000

18-SEP-2000

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25-SEP-2000

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25-SEP-2000

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29-SEP-2000

29-SEP-2000
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cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL70110 standard; DNA; 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pancreas cancer related gene sequence SEQ ID NO:8447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL70110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGTATGTTCAAGGTTGTGGAGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTTGCTGCAAGATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGGTTGTCCGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACTGGTGTAATGATGGCAAAACCCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAACTACAATGCTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGC
                       2000US-209473P.
2000US-209473P.
2000US-23403P.
2000US-23409P.
2000US-234052P.
2000US-234507P.
2000US-234567P.
2000US-234567P.
2000US-234567P.
2000US-234567P.
2000US-234567P.
2000US-235082P.
2000US-235082P.
2000US-23573P.
2000US-23573P.
2000US-23573P.
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2000US-23573P.
2000US-23563P.
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2000US-23603P.
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL6164 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, opesophageal, ovarian, kidney, prostate or pencreatic cancer.
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03-OCT-2000;
03-OCT-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 8447; 44pp; English
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03-OCT-2000;
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             301
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                                                                                                                                                                      134
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                                                                                                                                                                                                                                                                                                                                                               349;
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                                                                                                                                                                                                                                                                                                 14
                                                                                                                                                                                                                                                                                                                                                                            Similarity
GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA-
                                       TACTGGTGTAATGATGGCAAAACCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGT
                                                       TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                       GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCT
                                                                                                                                                                                                                                                                                                         ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                   ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                     ATGAGCCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCT
                                                                                                                                                                                                                                                              TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                            ATGAAGGCTCTCATTGTTCTGGGGGCTTGTCCTCCTTTCTGTTACGGTCCAGGGCAAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                      748 BP; 215 A; 138 C; 169 G; 226 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Augustus M, Weaver Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-237316P.
2000US-237425P.
2000US-237598P.
2000US-237604P.
2000US-237606P.
2000US-237606P.
2000US-244667P.
2000US-245084P.
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2000US-237294P.
2000US-237295P.
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2000US-237173P.
                                                                                                                                                                                                                                                                                                                                                                          62.8%;
78.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carter
                                                                                                                                                                                                                                                                                                                                                       Score 279; DB 24;
Pred. No. 4.3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĸc,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ebner
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                                                                                                                                                                                                                                                                                                                                                                                       Length 748;
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                                                                                                                                         Matches
                                                                                                                                                                Query Match
                                                                                                                                                                                                             A cDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and pHL8 (contg. a 300 bp insert).
                                                                                                                                                                                       Sequence 490 BP; 122 A; 100 C; 149 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                            New hybrid plasmids contg. sequences for human lysozyme - u e.g. as antiviral and antibacterial agent, and transformed
                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1987-136923/20.
                                                                                                                                                                                                                                                                                                                                                                                                        Sledziewski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DE3540075-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN70949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence encoding human lypozyme (HLZ) on cDNA clone HL14-1.
                                                                                                                                                      Local
128 TGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 GCTTTGCTGCAAGATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGGTTGTCCGTGAT
                                  15 CCCCCATTGTTCTGGGGCTTGTCCTCCTTTCTGTTACGGTTCAAGGCAAGGTCTTTGAAA
                                                                                                 8 CTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA
                                                                                                                                                    Similarity
                                                  GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA; 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTATGTTCAAGGTTGTGGAGTGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC 417
                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          85DE-3540075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiviral; bacteriolytic; phagocytosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                          Chlebowicz-Sledziewska
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85DE-3540075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
19..454
                                                                                                                                                   60.9%;
                                                                                                                                       0,
                                                                                                                                                  Score 270.4; DB 8; Pred. No. 1.7e-73;
                                                                                                                                       Mismatches
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TAGCAAACTGGATGTTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACT

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                    Sequence contained in plasmid pHLZ100. Apart from the four N-terminal amino acids, it encodes the entire sequence of human pre-lysozyme C of placental origin in addition to a translational stop signal. The mature lysozyme C corresponding to the pre-lysozyme C encoded by AAN92054 has the same AA sequence as human milk lysozyme. AAN92054 differs from the nucleotide sequence of the cDNAs encoding human pre-lysozyme C isolated from human histlocytic lymphoma cell line[U-937 (see FT tags a and b). However, these nucleic acid differences do not alter the amino acid
                                                                                                                                                                                                                                                                                                                                                             Prodn. of animal lysozyme C from pichia pastoris by secretion consists of P. pastoris promoter and terminator DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-NOV-1987;
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                                                                                                                                                                                                                                                                              Page 56; ; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams ME;
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Search completed: July 5, 2003, 05:31:23 Job time : 181 secs

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ALIGNMENTS

Dept of AFNS, University of Alberta 10 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada 11 780 492 0169 12: 780 492 4265 13: 780 492 4265 14: 5moore@afns.ualberta.ca 15: 5mail: smoore@afns.ualberta.ca 16: 5mail: smoore@afns.ualberta.ca 17: 6mail: smoore@afns.ualberta.ca 17: 6mail: 5moore@afns.ualberta.ca 18: 6mail: 5moore@afns.ua	REFERENCE 1 (bases 1 to 453) AUTHORS Moore, S.S., Hansen, C., Li, C., Fu, A., Meng, Y. and Li, G. TITLE cDNA's from bovine abomasum tissue JOURNAL Unpublished (2001) COMMENT Contact: Dr. Stephen Moore Beef Committee Taboratory	ACCESSION 86937925 VERSION BG937925.1 GI:14337297 VERSION BG937925.1 GI:14337297 KEYWORDS EST. SOURCE cow. ORGANISM Bos taurus ORGANISM Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	453 bp mRNA linear 4 Bovine Abomasum cDNA Library Bos taurus cE
P5, Canada zyme 7A mRNA f 0.0		eleostomi; Bovoidea;	EST 11-JUN-2001 NA 5', mRNA

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SUMMARIES

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BG937925 1Abo09H04 BG938107 1Abo11D05 BG938377 1Abo16E03 BG938413 1Abo07G10 BG938412 1Abo11D12 BG937589 1Abo03C3

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REFERENCE
AUTHORS
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                                                                                                                                                                                         sequence.
BG938107
MOORE, S.S., Hansen, C., Li, C., Fu, A
CDNA's from bowine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                           EST
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                                                                             Bovidae; Bovinae; Bos.
                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                           Bos taurus
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/lab_host="XIJ-BlueMRF/-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
87 c 121 g 116 t
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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Pred. No. 4.9e-125;
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BG938377
BG938377.1
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Seg primer: T3 primer
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High quality sequence stop:
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                                                                                                                                        TACGTTGAGGGTTGCACCCTGTAA
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
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/cell_type="Epithelial"
/dev_stage="Young adult"
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/db_xref="taxon:9913"
/clone_lib-"Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
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GI:14337749
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Pred. No. 4.9e-125;
Mismatches 0;
                                                             463 bp
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
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Contact: Dr. Stephen Moore
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                                                  CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                                                        GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG 360
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/cell_type="Epithelial" |
/dev_stage="Young adult" |
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/db_xref="taxon:9913"
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
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/sex="Two males and one female mixed"
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Pred. No. 4.9e-125;
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                                                                        194 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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Moore, S.S., Hansen, C., Li, C., Fu, A.,
cDNA's from boyine abomasum tissue
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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TGGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                  TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
                                                                                         ACABACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'.strain"
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92 c 121 g 119 t
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/db_xref="taxon:9913"
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Pred. No. 4.9e-125;
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410 Agr1/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Dr. Stephen Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 930.0 and E-value of 0.0
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
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/sex="Two males and one female mixed".
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I; Site_2: Xho I"
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High quality sequence stop:
POLYA=NO.
                                                                                                                                                                                                                                                                                                                                                                                                                 Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                          BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                         Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 944.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 476)
Moore, S.S., Hansen, C., Li, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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               135
         /dev_stage="Young adult"
/lab_host="Young adult"
/lab_host="YXL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
94 c 122 g 125 t
                                                                                                     /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
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                                                                                                                                                                                                /organism="Bos taurus"
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Score 444;

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Length 476;

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RESULT 7
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BG938203.1
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                                                                                                                                                                                                     Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                           MOORE, S.S., Hansen,C., Li,C., Fu,A., CDNA's from bovine abomasum tissue Unpublished (2001)
Contact: Dr. Stephen Moore
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1Abo13G08 Bovine Abomasum
                                                                                                 Seq primer: T3 primer
                                                                                                                  BACKWARD: M13
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1 (bases 1 to 476)
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                                                                         POLYA-No
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                                                                                                                                               PCR PRimers
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                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
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                                                                                    quality sequence
             /organism="Bos taurus"
/db_xref="taxon:9913"
                                                       Location/Qualifiers
/clone_lib="Bovine Abomasum
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                                                    sequence.
BG937601
Bos taurus
                                        BG937601.1
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1Abo03H1 Bovine Abomasum
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
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/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
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Pred. No. 5e-125;
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REFERENCE
AUTHORS
                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                      TITLE
                                                                    Unpublished (2001)
Contact: Dr. Stephen Moore
Deef Genomics Laboratory
Dept of AFNS, University of Alberta
A10 Agrifor, Dept of AFNS, U of A, E
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyia; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos. 1 to 478)
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 948.0 and E-value of 0.0
                                                                                                                                                                                                                                      cDNA's from bovine abomasum
                                                                                                                                                                                                                                         Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
                                                   Email: smoore@afns.ualberta.ca
                                                                                                                         Edmonton,
                                                                                                                                                                                                                                                            Meng,Y.
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BG937832.1
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                                    Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
    1 (bases 1 Moore, S.S.,
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1Abo07G03 Bovine
                               Bovidae; Bovinae;
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Seq primer: T3 primer
High quality sequence stop: 478
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FORWARD: M13 Forward
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/lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
95 c 123 g 125 t
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/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
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/cell_type="Epithelial"
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   Hansen, C.,
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BG937936 482 bp mrNA 1Abo08E01 Bovine Abomasum cDNA Library Bos
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: T3 primer
High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: smoore@afns.ualberta.ca
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ilarity 100.0%;
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/dev_stage="Young adult"
/lab_host="%IL1-BlueNEE'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
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/cell_type="Epithelial"
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/sex="Two males and one female mixed"
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Pred. No. 5e-125;
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DEFINITION

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11-JUN-2001

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Unpublished (2001)
Contact: Dr. Stephen Moore
. Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmc
Tel: 780 492 0169
Fax: 780 492 4265
Email: ***Commons**
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme )
in main database at high score of 955.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
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                                                                                                                                                                                                                                                                                                                                                                     CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                                                                                                                                            TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                              GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                            GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                          TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                     ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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136
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
96 c 123 g 127 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tssue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
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Pred. No. 5e-125;
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Mismatches
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                               181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCT
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372 CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 431
121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCCAGTTATAACACAAAAGCT 180
                                                                                             61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                14 ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                           1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
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1 (bases 1 to 484)
Moore,S.S., Hansen,C., Li,C., Fu,A.,
cDNA's from bovine abomasum tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG937881 484 bp mRNA linear EST 1
1Abo09C06 Bovine Abomasum cDNA Library Bos taurus cDNA 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 959.0 and E-value of 0.0
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/lab_host="Xil-BlueMRE'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
97 c 123 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIP)"
/cell_type="Epithelial"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine_Abomasum_cDNA_Library"
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Pred. No. 5e-125;
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cDNA's from bovine abomasum
Unpublished (2001)
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410 Agri/For, Dept of AFNS, U of A,
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Fax: 780 492 4265
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Bovidae; Bovinae; Bos.
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            ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
TACGTTGAGGGTTGCACCCTGTAA 444
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                                                     Conservative
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/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
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/sex="Two males and one female mixed"
                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
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97 c
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                                               Score 444; DB 13;
Pred. No. 5e-125;
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BG937882
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cDNA's from bovine abomasum tissue Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Ev
Tel: 780 492 0169
Fax: 780 492 4265
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BACKWARD: M13 Reverse
Seq primer: T3 primer
H1gh quality sequence s
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                                                                                                                                                                                                                                                                                                                                                                                                           The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 963.0 and E-value of 0.0
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1Abo09C07 Bovine Abomasum
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
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                                                                                                                                                                                                                                                                                                quality sequence stop:
                                                                                       /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="dastrointestinal tissue (GI
/cell_type="Epithelial"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: Ecor
I; Site_2: Xho I"
                                          /dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
                                                                                                                                                                                   /db_xref="taxon:9913"
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                      organism="Bos taurus"
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                                                                                                                                                 Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, EG
Tel: 780 492 0169
Fax: 780 492 4265
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1Abol1C10 Bovine Abomasum
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                 POLYA-No.
                                           Seq primer: T3 primer
                                                      BACKWARD: M13 Reverse
                                                                                                    The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 963.0 and E-value of 0.0
                                                                           FORWARD: M13 Forward
                                                                                                                                   Email: smoore@afns.ualberta.ca
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actyla; Ruminantia; Pec
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                                        MOOTE,S.S., Hansen,C., Li,C., Fu,A.
CDNA's from bowine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
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Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Tel: 780 492 0169
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I; Site_2: Xho I"
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|organism="Bos taurus"
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                                                                                                                                                 ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Email: smoore@afn:
                                                                 TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                     mail: smoore@afns.ualberta.ca
he sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA
in main database at high score of 985.0 and E-value of 0.0
                                                                                                                                   CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
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// Site_2: Xho I"
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US-08-385-590A-3

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US-09-786-023-3

US-09-786-923-3

US-09-388-917-2

US-08-32-463-14

US-08-32-463-14

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Sequence 344, App
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US-07-798-223A-1
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STATE: Illinois
COUNTRY: USA
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98.9%; Score 439; DB 1; Lo 100.0%; Pred. No. 1.5e-133; tive 0; Mismatches 0;

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Sequence 3, Appli	Sequence 22, Appl	Sequence 1553, Ap	Sequence 6, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 97, Appl	•			Sequence 98, Appl		Sequence 98, Appl	•				

ALIGNMENTS

Sequence 1, Application US/07798223A Patent No. 5422108 GENERAL INFORMATION: CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION UMBER: 07/762,679 FILLING DATE: 19-SEP-1991 ATTORNEY/ACENT INFORMATION: NAME: Seidman, Stephanie L. REGISTRATION UMBER: 33,779 REFERENCE/DOCKET NUMBER: 51984 TELECOMMUNICATION INFORMATION: TELECAX: (619)552-1311 TELECAX: (619)552-1311 TELEFAX: (619)552-0091 ZIP: 60603 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy APPLICANT: Mirkov, T. Erik APPLICANT: Fitzmaurice, Leona Claire TITLE OF INVENTION: Protection of Plants Against Pathogens NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDERFECT CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 964 base pairs MOLECULE TYPE: cDNA LENGTH: 964 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: unknown APPLICATION NUMBER: UPFILING DATE: 19911125 ADDRESSEE: Fitch, Even, Tabin & Flannery STREET: 135 South LaSalle Street, Suite 900 Floppy disk US/07/798,223A

314 313 254 253

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GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: WOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX

CURRENT APPLICATION NUMBER: U$/09/385,982

CURRENT FILING DATE: 1999-08-30

EARLIER APPLICATION NUMBER: 60/328,111

EARLIER APPLICATION NUMBER: 60/117,393

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 60/098,639

EARLIER FILING DATE: 1998-01-27

EARLIER FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 544

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 344

LENGTH: 657
                 Q
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                                                                                                                        Similarity
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                                             TTGTTCTGGGGCTTGTCCTCTTTCTGTTACGGTCCAGGGCAAGGTCTTTGAAAGGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09385982
                                                                                                           Conservative
                                                                                                                      56.3%;
75.9%;
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                                                                                                        0;
                                                                                                     Score 250; DB 4; L
Pred. No. 5.2e-72;
0: Mismatches 97;
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                                                                                                                                     Length 657;
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                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Patent No. 5182195
; APPLICANT: NAKAHAMA, KAZUO; KA
; TITLE OF INVENTION: METHOD FC
; DEFICIENT YEASTS
; NUMBER OF SEQUENCES: 71
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/
; FILING DATE: 09-NOV-1988
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 394
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                               GTTACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                                                                                                                                                                                                                                                                TTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAG 121
              AATACGTTCAAGGTTGTGGTGTTTAA
                                                                        CACAGGGTATTAGAGCCTGGGTCGCTTGGAGAAACAGATGCCAAAATAGAGATGTCAGAC
                                                                                                                                 CTTTGCTTCAGGACAACATTGCTGATGCTGTTGCCTGCGCTAAGAGAGTTGTCCGTGACC
                                                                                                                                                    AATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA--
                                                                                                                                                                                              ATTGGTGTAACGATGGCAAGACTCCAGGTGCCGTCAACGCCTGTCACTTATCTTGCTCAG
                                                                                                                                                                                                             GGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCG
                                                                                                                                                                                                                                                                                                                                                                               TCGAGAGATGCGAATTAGCCAGAACTTTGAAGAGATTGGGTATGGACGGCTACCGTGGTA 60
                                                                                        -GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCA 418
                                                                                                                                                                                                                                                                                                                    TTTCTTTAGCCAACTGGATGTGTCTTGCTAAGTGGGAATCCGGCTATAACACTAGAGCTA
                                                                                                                                                                                                                                                                                                                                                 TCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAGCCATGACGTCAGCAGTTACGTTGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTC----AGTGAGCAAGGCAT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAACATCGCTGATGCTGTAGCTTGTGCAAAAAANGGTTGTCCCGTGATCCACAAGGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.4%;
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METHOD FOR INCREASING USING PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/269,140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence b,
                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Nakaji
APPLICANT: Oheda,
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: JP-165266/1994
FILING DATE: 18-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP-276573/1994
FILING DATE: 11-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, Leonard R.
NAME: SVENSSON, Leonard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IShige, Fumiharu
TITLE OF INVENTION: method;
TITLE OF INVENTION: resistai
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US/01
FILING DATE: 18-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                  OLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
124 AGAGCTACTAACTACAACGCCGGTGACCGTTCTACTGACTACGGTATCTTCCAAATTAAC
                                  175 AAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAAC 234
                                                                                                          115 AAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACA 174
                                                                                                                                                                                                                    250;
                                                                                                                                                               55 AAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTAT 114
                                                                        64 CGTGGTATCTCTTTGGCTAACTGGATGTGTTTTGGCCAAGTGGGAATCTGGTTACAACACT
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                                                                                                                                            4 AAAGTTTTCGAACGTTGTGAATTGGCCAGAACTTTGAAGAGATTGGGTATGGACGGTTAC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Falls Church
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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110 Gatehouse Road, Suite 500 Eas
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                           peptide
1 to 393
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                  nonnatural type
                                                                                                                                                                                                                                                                                                                                                                                                                     Other nucleic acid
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                                                                                                                                                                                                                                     34.5%;
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Pred. No. 1.7e-40;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic DNA of
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                                                                                                                                                                                                                      140;
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US-08-385-590A-3
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                                                                                                                                 Matches
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                TELEFAX: (716) 263-160
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 5824861e111, John L.
TITLE OF INVENTION: TRANSCENIC POMACEOUS FRUIT WITH FIRE
TITLE OF INVENTION: BLIGHT RESISTANCE
                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/385,590A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412 GTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 CGCGACCCACAAGGTATCCGTGCTTGGGTCGCTTGGCGTAACCCGCTGTCAAAACCGTGAC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AGTGA---GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGAC 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 AGCAAATGGTGGTGAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 GTGCCTCAATACGTTCAAGGTTGTGGTGTCTAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TGTTCTGCTTTGTTGCAAGACAACATCGCTGACGCCGTTGCCTGTGCTAAACGTGTCGTT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 TCTAGATACTGGTGTAACGACGGTAAGACTCCAGGCGCCGTTAACGCCTGTCACTTGTCT 243
                                                                                                                                 258;
61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGGA 120
                                                     30 ATGAGGTCTTTGCTAATCTTGGTGCTTTGCTTCCTGCCCCTGGCTGCTCTGGGGAAAGTC 89
                                                                           1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14603
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                                                                                                                                                                                                                                                                                                      586 base pairs
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  (716) 263-1304
                                                                                                                                                                                                                             DNA (genomic)
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57.7%;
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                                                                                                                                                   Score 122.2; DB 1
Pred. No. 2.3e-30;
                                                                                                                                   Mismatches 183;
                                                                                                                                                                       DB 1;
                                                                                                                                       Indels
                                                                                                                                                                       Length 586;
                                                                                                                                       6
                                                                                                                                       Gaps
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57.7%;

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US-09-021-520-3
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US-09-021-520-3
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    Query Match
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                                                                                                                                            TELEFAX: (716) 263-16(
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                               MOLECULE TYPE:
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 586 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 6100453elli, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
TITLE OF INVENTION: BLIGHT RESISTANCE
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                              STRANDEDNESS:
                                                                                                                                                                                                                 NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Rochester
STATE: New York
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Nixon, Hargrave, Devans & Doyle LLP
Clinton Square
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                                               DNA (genomic)
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Score 122.2;
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LENGTH: 222
TYPE: DNA
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; ORGANISM: Gallus gallus US-09-388-917-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09388917 Patent No. 6258542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/388,917
CURRENT FILING DATE: 1999-09-02
EARLIER APPLICATION NUMBER: 10-250619
EARLIER FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hayashizaki, Yoshihide
TITLE OF INVENTION: Method for Supporting DNA-Fixation and DNA-Fixed
TITLE OF INVENTION: Support
FILE REFERENCE: 1794-0120P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 11-240910
EARLIER FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn
                         121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 GCGTGGATCAGAGGCTGCCGGCTGTGA 473
                                                                                                                            61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                               32 ATGAGGTCTTTGCTAATCTTGGTGCTTTGCTTCCTGCCCCTGGCTGCTCTGGGGAAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
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                                                                                                                                                                                                                                                                                                                                Similarity
                                                                      TTTGGACGATGTGAGCTGGCAGCGGCTATGAAGCGTCACGGACTTGATAACTATCGGGGA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGC 417
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Conservative
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<u>-</u>
                                                                                                                                                                                                                                                                                                                             Score 63.8; DB 4; Pred. No. 1.6e-11;
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Sequence 2, Application US/09388917 Patent No. 6258542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Zhao, Yong
APPLICANT: B1, Anding
TITLE OF INVENTION: A NOVEL HUMAN LYSOZYME GENE, ITS ENCODED
TITLE OF INVENTION: POLYPEPTIDE AND THE METHOD FOR PREPARING
FILE REFERENCE: A34053-PCT-USA
CURRENT EPPLICATION NUMBER: US/09/786,023
CURRENT FILING DATE: 2001-06-21
CURRENT FILING DATE: 2001-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-786-023-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/CN99/00131
PRIOR FILING DATE: 1999-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yu, Long APPLICANT: Fu, Qia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (106)...(552)
NAME/KEY: variation
LOCATION: (79)...(79)
OTHER INFORMATION: A, C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: variation LOCATION: (88)...(88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: A, C, G or T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 TTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAAAAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 TACAGCCTGGGAAACTGTAAGTCTGTATTCTCATG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 TATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCCTTCAGCCTTGGAAACTGGATCTGCA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 TTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTGAGCTTGCCAGAA 85
                                                                                                               GCTGGAAGAAACATTGTGAGGGCAGAGACCT
                                                                                                                                                    CATGGAAAAGTCATTGTCGAGACCATGACGT 413
                                                                                                                                                                                                                         AAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG----CAAGGCATTACAGCCTGGGTGG 382
                                                                                                                                                                                                                                                                  TGAAGGAGAACCACCTGCCACGTCGCCTGCTCAGCCTTGATCACTGATGACCTCACAG
                                                                                                                                                                                                                                                                                                     CTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTA 325
                                                                                                                                                                                                                                                                                                                                          GCATCGACTACGGCATCTTCCAGATCAACACGTTCGCGTGGTGCA---GACGCGGAAAGC
                                                                                                                                                                                                                                                                                                                                                                       GCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGATGGCAAAACCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                TGGCATATTATGAGAGCGGCTACAACACCACAGCCCCAGACGGTCCTGGATGACGGC---A 310
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGACCAAATGGGAAAGCAGTTATAACACAAAAAGCTACAAACTACAATCCTAGCAGTGAAA 205
                                                                                                                                                                                         ATGCAATTATCTGTGCCAGGAAAATTGTTAAAGGAGACACAAGGAATGAACTATTGGCAAG
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52.9%;
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Pred. No. 4.6e-11
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22313-0299
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les 86; Conserv
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Alexandria
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LENGTH: 301
TYPE: DNA
ORGANISM: Gallus gallus
US-09-388-917-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 11-240910 EARLIER FILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-09-04
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                     APPLICATION NUMBER: FILING DATE: 26-AUG
                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 GCAGGACCCC 210
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o. 5670367
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llarity 66.2%;
Conservative
                                                                                                                                          26-AUG-1991
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Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 500
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RESULT 11
US-08-385-590A-1
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INFORMATION FOR SEQ ID NO:
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE TITLE OF INVENTION: BLIGHT RESISTANCE
                                                                                                                                                                                                                                                                                                                       APPLICANT: Aldwinckle, Herbert S. APPLICANT: No. 5824861elli, John L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                            APPLICATION NUMBER: US/0 FILING DATE: 08-FEB-1995
   APPLICATION NUMBER:
                               CLASSIFICATION:
                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                     CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 CAAGGCAAGGTCTTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGAC 108
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Clinton Square
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US 07/954,347
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Pred. No. 0.0005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09021520 Patent No. 6100453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,520
PRIOR APPLICATION DATA:
                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                    APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 6100453e1l1, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
TITLE OF INVENTION: BLIGHT RESISTANCE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                     FILING DATE
                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   CLASSIFICATION:
                                                                                             SOFTWARE:
                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                         ZIP:
                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Goldman, Michael REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 AAAATCACTGTCAACA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 GAGACTACGGCCTCTTCCAGATCAATGACAATACTGGTGCAGTAAGGGATCCACTCCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 AAAGTCATTGTCGAGA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 ATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 TGCAGGAGCTTAGGAGACGAGGCTTCGATGAAACTTTGATGAGTAACTGGGTCTGCCTTG 118
                                                                                                                                                                                           14603
                                                                                                                                                                                                                                              Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
DEDNESS: double
                                                                                                                                                                                                                            New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 base pairs
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                                                                                         PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                               Nixon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.3%;
                                                                                                                                                                                                                                                                                   Hargrave, Devans & Doyle LLF
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30,727
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Pred. No. 0.00048;
0; Mismatches 158;
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                                                                                           #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158;
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US-08-449-644-3/c
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US-09-021-520-1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08449644 Patent No. 5856162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Schles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASE-KAPPA NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              APPLICANT: Vogel, Wolfgang APPLICANT: Fuchs, Miriam
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                            STREET: 1155 A
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                                                                                                                     COUNTRY: U.S.A. ZIP: 10036
                                                                                                                                                          STATE: New York
                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 AAAGTCATTGTCGAGA 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGCTACGTGCGCGAAGAAGATTTACAAACGCCACAAGTTTGACGCTTGGTACGGATGGA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAATCACTGTCAACA 368
                                                                                                                                                                                        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                    Sap, Jan M.
Ullrich, Ax
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                                                                                                                                                                                                                PENNIE & EDMONDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.2; | DB 3; Pred. No. 0.00048;
                      #1.25
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US-08-087-244A-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.3%;
Best Local Similarity 45.5%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-8864/
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                    COMPUTER READABLE FORM:
                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE TITLE OF INVENTION: PHOSPHATASE-KAPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                           STREET: 1155 Av
CITY: New York
STATE: New Yorl
                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/087,244 FILING DATE: 01-JUL-1993
                                                                                                 ADDRESSEE: PENNIE & ELFRONCE
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4374 base pairs
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Coruzzi, Laura A.
74
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                                                                             New York
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Fuchs, Miriam
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Ullrich, Axel
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                                                        U.S.A.
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Pred. No. 1.3;
0; Mismatches 138;
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Gaps

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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 15
US-09-440-325A-2/c
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                                                                                                   SOFTWARE: FastSEQ for Windows
SEQ ID NO 2
LENGTH: 2082
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09440325A Patent No. 6280994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.3%;
Best Local Similarity 45.5%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/440,325A
CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: Zacl: A Human Metalloenzyme
FILE REFERENCE: 98-79
                   FEATURE:
OTHER INFORMATION: This degenerate sequence encodes the amino OTHER INFORMATION: sequence of SEQ ID NO:1.
               NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4374 base pair
LOCATION: (1)\dots(2082)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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LOCATION:
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TELEPHAX: 212-869-8864/9741
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/087,244A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3329 TAACAGCCTGTGC 3317
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DEDNESS: double
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Pred. No. 1.3;
0; Mismatches 138;
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US-09-440-325A-2
Search completed: July Job time: 43 secs
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                                                                                                                                                                                                                                                             7.28;
Local Similarity 31.28;
les 39; Conservation
                                                                  329 GCYTG 325
                                                                                                   125 GCCTG 129
                                                                                                                                 389 ARYTTNSWNARCATNCCRTTNACRTCNGGRTCYTTRAAYTGNGTNACYTTRAANARRTGN 330
                                                                                                                                                                                                   449 ARNARYTCRTTRTAYTCNCKNARYTCRTCYTTNSWNARNGCNGCYTTRTCDATRTTYTGN 390
                                                                                                                                                                65 AGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCA 124
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                 2003, 06:17:01
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Pred. No.
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Minimum DB seq length: 0
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA:*
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_EUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_EUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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36.8	36.8	38.9	38.9	38.9	38.9	38.9	41.8	41.8	41.8	42.8	56.3	59.7	60.3	60.3	60.3	62.8	100.0	100.0	Query Match
233	233	636	636	522	367	367	582	582	582	606	657	2467	478	478	478	748	10132	444	Query Match Length
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US-09-895-828-117	US-10-114-666-117	US-10-040-862-8226	US-09-796-692-8226	US-10-102-524-791	US-10-040-862-8055	US-09-796-692-8055	US-10-146-502-1606	US-09-878-178	US-10-046-935-1606	US-10-060-036-2544	US-09-871-161-344	US-10-001-873-11	US-10-146-502-1085	US-09-878-178-1085	US-10-046-935-1085	US-09-969-347-318	US-09-978-199-3	us-09-978-199-1	ID , _
8-117	-117	-8226	-8226	-791	-8055	-8055	-1606	-1606	-1606	-2544	-344	-11	-1085	-1085	-1085	7-318	9-3	9-1	1 1 1 1 1
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Sequence 117, App	Sequence 117, App	Sequence 8226, Ap	Sequence 8226, Ap	Sequence 791, App	Sequence 8055, Ap	Sequence 8055, Ap	•	Sequence 1606, Ap	Sequence 1606, Ap	Sequence 2544, Ap	Sequence 344, App	Sequence 11, Appl	Sequence 1085, Ap	Sequence 1085, Ap	Sequence 1085, Ap	Sequence 318, App	Sequence 3, Appli	Sequence 1, Appli	Description

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US-09-978-608A-220	10-:	10-	10-	10-	10-137-865-407	10-	10-3	10-175-746-407	10-3	10-1	10-1	10-0	JS-09-978-189-220	US-09-999-832A-220	9-60	JS-09-978-697-220	JS-09-978-295A-220	US-10-040-862-8818	7-60	US-09-833-263-526	US-09-922-217-526	-01	10-0	US-10-077-381-1	10-0
978	140	143-114	142.	140	137	176-	176	175-	140-	123	121	028-	978-	-666	378-	978-	978-	040-	796-	-833	922)25-	-990)77-)76-
-608	-002	-114	-431	-474	-865	-921	-918	-746	47C	904	049	072	189	832	·192	697	295	.862	692	3-26	2-21	380	.543	381	816
A-2	2-4C	4-407	4C	-4C	-40	-40	-40	-40) - 4 C	-40	-40	-40	-22	A-2	A-2	-22	A-2	88-	88-	3-5	7-5	-52	-31	Ļ	Ļ
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ALIGNMENTS

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APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 444; DB 10; Best Local Similarity 100.0%; Pred. No. 7.1e-134; Matches 444; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09978199 Patent No. US20020104126A1
                                                                                                                                                                                                                                                                                                             Matches 444; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 42202
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Bovine sp. FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 444
TYPE: DNA
                                                              181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                         121 GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                               61 TTTGAGAGACATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                                                                                     1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
Length 444;
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US-09-978-199-3
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TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
CURRENT EPILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 05/240,967
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
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Best Local
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TYPE: DNA
ORGANISM: Bovine sp.
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            TACGTTGAGGGTTGCACCCTGTAA 444
                                                              CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                                                      TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                             CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                                    TGGTGGTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 318
LENGTH: 748
                                                                                                                             RESULT 4
US-10-046-935-1085
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                                                                        Sequence 1085, Application Patent No. US20020156011A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign TITLE OF INVENTION: Sets
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                                                                                                                                                                                                    CAGTATGTTCAAGGTTGTGGAGTGTAA 460
                                                                                                                                                                                                                       AGTTACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                                                                                                                                                                                                                                                                           TACTGGTGTAATGATGGCAAAACCCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGT 313
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78.1%;
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Pred. No. 3.5e-80;
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-046-935-1085
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CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1085
LENGTH: 478
                                                                                                                                                                                                                                                                                                        Sequence 1085, Application US/09878178 Patent No. US20020177552A1 GENERAL INFORMATION:
                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1085
LENGTH: 478
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Query Match
                                                                                                                                                                                               APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
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APPLICANT: Harlocker, Susan L.
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                                                    TYPE: DNA
ORGANISM: Homo sapien
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78.0%;
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Pred. No. 1:2e-76;
Pred. No. 1:2e-76;
Score 267.8;
 DB
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LENGTH: 478
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                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harlocker, APPLICANT: Secrist, He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jiang,
                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                     Local Similarity
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137 GGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTA 196
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                                                     62 TGGCCAGAACTCTGAAAAGATTGGGAATGGATGGCTACAGGGGAATCAGCCTAGCAAACT
                                                                                         77 TTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACT 136
                                                                                                                                                2 TTCTGGGGCTTGTCCTCTTTCTGTTACGGTCCAGGGCAAGGTCTTTGAAAGGTGTGAGT 61
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Secrist, Heather
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0; Mismatches 92;
                                                                                                                                                                                                                     Score 267.8; DB 9
Pred. No. 1.2e-76;
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Sequence 11, Application US/10001873

Patent No. US20020160388A1

GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
ITILE OF INVENTION: Compositions and Methods Rel
CURRENT APPLICATION NUMBER: US/10/001,873

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/252,055

PRIOR APPLICATION NUMBER: 60/252,496

PRIOR APPLICATION NUMBER: 55

PRIOR FILING DATE: 2000-11-22

NUMBER OF SEQ ID NOS: 55

SOFFWEAR DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20

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SEQ ID NO 11
LENGTH: 2467
                                                                                                                                                                                                                                                                                                    Matches 345;
                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       Query Match
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NAME/KEY: misc_feature
LOCATION: (2319)..(2319)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapien
                                      186 CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
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                                                                                           126 CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
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                                                                        CCTAGCAAACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAA
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78.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(657)
; OTHER INFORMATION: n = A,T,C
US-09-871-161-344
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CURRENT FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 09/328,111
PRIOR APPLICATION NUMBER: 60/217,393
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: 60/098,639
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 657
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                          134 ACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATC 193
                                                                                                                                                 194 CTAGCAGTGAAAGCACTGATTATGGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATG
                 314 ATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTC----AGTGAGCAAGGCAT
                                                                                      254 ATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAA 313
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                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity 75.9
322; Conservative
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                                                                                                                                                                                                                                                                                               74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGGACTCAGCCTGGCAA 133
                                                                                                                                                                                                                                                                                                                                                15 TTGTTCTGGGGCTTGTCCTCTTTCTGTTACGGTCCAGGGCAAGGTCTTTGAAAGGTGTG
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                                                   ATGGCAAAACCCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAAG
                                                                                                                              CTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGCTACTGGTGTAATG
                                                                                                                                                                                                     ACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAATG
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Application US/09871161 o. US20030097666A1
                                                                                                                                                                                                                                                                                                                                                                                                                                            75.98;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 250; DB 9; Length 657; Pred. No. 8.4e-71; 0; Mismatches 97; Indels
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RESULT 10
US-10-046-935-1606/c
; Sequence 1606, Application US/10046935
; Patent No. US20020156011A1
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036 |
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2544
LENGTH: 606
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 603
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAG
                                                                                                                                                                  CATGACGTCAGCAGTTACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                         GTTGTCCGTGATCCACAAGGCATTAGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAAAC
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                                                                                                                                                                                                                                                ATTGTCAGTGA---GCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGAC
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76.48;
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Pred. No. 2.4e-51;
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                                                                                                                                                                    APPLICANT: Jiang, ruqiu

APPLICANT: Harlocker, Susan L.

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210121.527

CURRENT APPLICATION NUMBER: US/09/878,178

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 2237

SOFTWARE: FASSISEQ FOR Windows Version 4.0

SEQ ID NO 1606

LENGTH: 582
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                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-1606
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APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1606, Application US/09878178 Patent No. US20020177552A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.8%;
Best Local Similarity 76.5%;
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                                                        Query Match
Best Local Similarity
                                        Matches 241;
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ORGANISM: Homo
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133 AACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAAT 192
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                                        Conservative
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                                     Score 185.4; DB 9;
Pred. No. 7.4e-50;
0; Mismatches 71;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-1606
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US-10-146-502-1606/c
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TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
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APPLICANT: Harlocker, St
APPLICANT: Secrist, Heat
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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             430 GGTTGCACCCTGTAA 444
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                                                                                                                                                                                         402
                                                                                                                                                                                                                                                                                                    462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 AACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAAT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                               193 CCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAAT 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 GGTTGTGGAGTGTAA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        342 AGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGTCAGTATGTTCAA
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                                                                                                                                                                                                                                                                                                                                       GATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAA 312
                                                                                 AGAGCATGGGTGGCATGGAGAAATCGTTGTCAAAACAGAGATGTCCGTCAGTATGTTCAA 283
                                                                                                             ACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGGTTACGTTGAG 429
                                                                                                                                                                                    GATAACATCGCTGATGCTGTAGCTTGTGCAAAGAGGGTTGTCCGTGATCCACAAGGCATT
                                                                                                                                                                                                                                        AATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGA---GCAAGGCATT 369
                                                                                                                                                                                                                                                                                            GATGGCAAAACCCCCAGGAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAA 403
                                                                                                                                                                                                                                                                                                                                                                                                 GCTGGAGACAGAAGCACTGATTATGGGATATTTCAGATCAATAGCCGCTACTGGTGTAAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACTGGATGTGTTTGGCCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTGCACCCTGTAA 444
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Stolk, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.8%;
76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 7.4e-50;
0; Mismatches 71;
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/20,999
PRIOR APPLICATION NUMBER: 60/20,999
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/20,20,84
PRIOR APPLICATION NUMBER: 60/20,20,84
PRIOR APPLICATION NUMBER: 60/20,999
PRIOR FILING DATE: 2000-05-04
PRIOR PRILING DATE: 2000-05-04
PRIOR PRILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR PRICING DATE: 2000-08-04
PRIOR PRILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
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US-09-796-692-8055
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SEQ ID NO 8055
LENGTH: 367
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Best Local Similarity
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (361)
OTHER INFORMATION: n=A,T,C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                 149 CCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCA 208
                        329 CTGTAGCGTGTGCAAAGCATATTGTCAGTGA---GCAAGGCATTACAGCCTGGGTGGCAT
                                                                                                       269 ATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAG 328
                                                                                                                                                                                                          209 CTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGATGATGGCAAAACCCCTA 268
                                                                                                                                                                                                                                                                                                                                                                                              227;
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                                                                                                                                                                                                                                                                                      1 CCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAATGCTGGAGACAGAAGCA
                                                                         GAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAAGATAACATCGCTGATG
                                                                                                                                                                              CTGATTATGGGATATTTCAGATCAATAGCCGCTACTGGTGTAATGATGGCAAAACCCCAG 120
Conservative
                                                                                                                                                                                                                                                                                                                                                                                        38.9%; Score 172.6; DB 9; 75.9%; Pred. No. 8.1e-46; tive 0; Mismatches 69;
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SEQ ID NO 8055
LENGTH: 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILLING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILLING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2001-11-06
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                                                                                                                                                                                                                                NAME/KEY: unsure LOCATION: (361) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure LOCATION: (331) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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                                                                                                                               Local Similarity es 227; Conserv
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/223,378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/202,084 FILING DATE: 2000-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/796,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-08-07
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209 CTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGATGGCAAAACCCCTA 268
                                                               149 CCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 3.0
                                       CCAAATGGGAGAGTGGTTACAACACACGAGCTACAAACTACAATGCTGGAGACAGAAGCA
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Corixa Corporation
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                                                                                                                               Conservative
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                                                                                                                                               38.9%;
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                                                                                                                             0;
                                                                                                                         Score 172.6; DB 9
Pred. No. 8:1e-46;
0; Mismatches 69
                                                                                                                                                                   DB 9;
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US-10-102-524-791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAST AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 447, 456, 466
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 522
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                           386 GGAAAAGTCATTGTCGAGACCATGACGTCAGCACTTACGTTGAGGGTTGCACCCCTGTAA 444
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                                                                                                                                                                     121 GAGCAGTTAATGCCTGTCATTTATCCTGCAGTGCTTTGCTGCAAGATAACATCGCTGATG
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	RESULT 1 108277 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL			Result
	2 2			
	277 uence 277 277 277 1000 1000 1000 1000 1000 10		Match 100.0 100.0 100.0 98.4 98.4 98.4 98.5 98.4 98.5 98.4 98.5 98.5 37.5 21.6 21.6 21.6 21.6 21.6 21.6 21.6 21.6	Query
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	459 bp DNA 2 from Patent EP 0374913. GI:589012 ied. 1 to 459) storis glyceraldehyde-3-phosphate P 0374913-A1 2 27-JUN-1990; Location/Qualifiers	ALIGNMENTS	ID IO8277 BOVLSZ2B BOVLSZ17A I12256 BOVLSZ2A I103315 BOVLSZ2A BOVLSZ3A BOVLSZ3A BOVLSZ3A BOVLSZ3A BOVLSZ3A BOVLSZ3A BOVLSZ3A BOVLSZ1B SHPLZM1A AXILZM1 AXILZM1 AXILZM2 BOVLXSOZMA BTU19466 SHPLZM3A BTU19466 SHPLZM3A BTU19466 BOVLZSMA BTU19466 BOVLZSMA BTU19461 BTU1	
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Irwin,D.M. and Wilson,A.C.
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                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                .M.Irwin,
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            /protein_id="AAA30629.1"
/db_xref="GI:163317"
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1 89 c 119 g
                                  /codon_start=
                                            /note="lysozyme
                                                                  /db_xref="taxon:9913"
translation="MKALVILGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLA"
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                                                                                                                                                                         Multiple cDNA sequences of bovine tracheal lysozyme J. Biol. Chem. 268 (36), 27440-27446 (1993) 94086565
                                                                                                                                                                                                                                 Takeuchi, K., Irwin, D.M., Gallup, M., Shinbrot, E., Stewart, C.B. and Basbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus lysozyme
L23758
L23758.1 GI:387905
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1 (bases 1 to 1060)
                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (cow).
                                                                                                                                                                                                                                                                                                                                                                                       lysozyme.
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 þ
 /dev_stage="adult"
181 c 223 q
                                   /organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="epithelial/
/tissue_type="trachea"
                                                                                                                                     Location/Qualifiers
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162 c 194 g
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73. .459
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                                                                                                                                                                                                                                                                                     Mirkov, T. Erik. and Fitzmaurice, L.C. Protection of plants against plant Patent: US 5422108-A 1 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                               Unclassified.
                                                                                                                                                                                                                                                                                                                                                            Unknown
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CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA 185
                                          GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 143
                                                                      GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                 GGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
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ilarity 100.0%;
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Pred. No. 5.5e-246;
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68 GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
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M26241 J04831 M27181
M26241.1 GI:163314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases i to 909)
Irwin, D.M. and Wilson, A.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                            CTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA 62
                                                         CTCTCGTTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA 67
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                                                                                                                                                                                                                                                                                                                                                                                                                   .M.Irwin,
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   entry and computer-readable M.Irwin, 23-JUN-1989.
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                                                                                                                                                                                                  /note="lysozyme 2a signal peptide"
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                                                                                                                                                                     /product="lysozyme
154 c 187 g
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                                                                                                                                                                                                                                            NDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL'
                                                                                                                                                                                                                                                         /protein_id="aaa30628.1"
/db_xref="GI:163315"
/translation="TlvIlGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGVSLANW
/CLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELME
                                                                                                                                                                                                                                                                                                                /codon_start=2
                                                                                                                                                                                                                                                                                                                             /note="lysozyme 2a precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Digan, M.E., Harpold, M.M., Lair, S.V., Thill, G.P., Siegel, R.S., Ellis, S.B. and Williams, M.E. PRODUCTION OF ANIMAL LYSOZYME C VIA SECRETION FROM PICHIA PAS
                                                                                                                                                                                                                                                                                                                                                                                                                       Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified
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  ACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGT
                                                                                                                                                                        GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
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                                                                                                                                                                                                                                 CTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA
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llarity 100.0%; Pred. No. 8.2e-245;
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                                                                                                               65 GCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATA
                                                                                                                                                                                                   50
                                                                                                                                                                    Draft entry and computer-readable sequence by D.M.Irwin, 23-JUN-1989.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multiple cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecayidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
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M26244 J04831 M27183
M26244.1 GI:163318
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Irwin, D.M. and Wilson, A.C.
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                                                                                                                                                                                                                            Similarity 100.
95; Conservative
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              TCAACAGCAAATGGTGGTGAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATG
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TCAACAGCAAATGGTGGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATG
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                                                         ACACAAAAGCTACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGA
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                                                                                                                                                                                                                                                                                                                              /note="lysozyme 2c signal peptide"
10. .396
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                                                                                                                                                                                                                                                                                                  /product="lysozyme 2c"
142 c 181 g
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/db_xref="taxon:9913"
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/db_xref="GI:163319"
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                                                                                                                                                                                                                           89.0%; Score 395; DB 4; Lo
100.0%; Pred. No. 3.8e-220;
Live 0; Mismatches 0;
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              247
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                                                                                                                                                                                                                    195 TAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGA
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M26240 J04831 M27184
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1 (bases 1 to 786)
Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine abomasum, cDNA to mRNA, clone lambda-cBL29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGTCAGTGAGCAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATA 349
                            CTGGGTGGCATGGAAAAGTCATTGTCGAGACCCATGACGTCAGCAGTTACGTTGAGGGTTG
                                                                          TGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGGCATTACAGC
                                                                                                                                                      TGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAA 314
                                                                                                                                                                                                     TAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGA 126
                                                                                                                                                                                                                                                                  CTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATCC
                                                                                                                                                                                                                                                                                 CTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACCTACAATCC 194
              CTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGTTGAGGGTTG
                                                                                                                                     TGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.M.Irwin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 264 (19), 11387-11393 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                             256
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry and computer-readable M.Irwin, 23-JUN-1989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAA30631.1"|
/db_xref="G1:163321"
/tanslation="ASWICCLTKWE$SYNTKATNYNPSSESTDYGIFQINSKWWCNDGK
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TPNAVDGCHVSCSELMENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                             127 c
                                                                                                                                                                                                                                                                                                                                           69.8%; Score 310; DB 4; Length 786; 100.0%; Pred. No. 3e-170;
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                                                                                                                                                                                                                                                                                                                                                                                                           154 g
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Best Local
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||||||||||
307 CACCCTGTAA 316
                                                                                                                                                                                                       142
                                                                                             254 ATGGCAAAACCCC 266
                                                                                                                                        202
                                                                                                                                                         194 CTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATG
                                                                             262
                                                                                                                                                                                                                                     134 ACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACTACAATC
                                                                                                                                                                                                                                                                                                                                                                                                252;
                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                 74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCAA 133
                                                                                                                                                                                                                                                                                                                               22 TTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG
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Bovine lysozyme c isozyme 3a mRNA, complete cds.
M26242 J04831 M27180
M26242.1 GI:163322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable sequence for by D.M.Irwin, 23-JUN-1989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1082)
Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lysozyme.
BOYLYSOZMB
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                                                                                                                                        CTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATG
                                                                                                                                                                                                     AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGATGGCTATAAGGGAGTCAGCCTGGCAA
                                                                           ATGGCAAAACCCC 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="lysozyme 3a signal peptide"
63. .449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAA30632.1"
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/translation="MKALILIGELFLSVAVOGKVFERCELARTLKKLGLDGYKGVSLA
NWLCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="lysozyme 3a"
205 c 209 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="lysozyme 3a precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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99.6%;
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Pred. No. 7.8e-107;
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   MAM 29-OCT-1993
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253

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BASE COUNT
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ACCESSION
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Irwin,D.M., White,R.T. and Wilson,A.C.
Characterization of the cow stomach lysozyme genes: repetitive DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus
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        3031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taurus lysozyme gene (cow 2), complete cds
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_Evol. 37 (4), 355-366 (1993)
                     /label=exon4
                                          /number=
                                                      /note="putative"
                                                                       /label=exon3
7575. .8130
/gene="lysozyme"
                                                                                                                                                                                                                                                                                                                                                    /rpt_type=dispersed
4381. .4510
                                                                                                                                                                                                                                                                                                                                                                          4113. 4238
/gene="1ysozyme"
/note="putative"
/rpt_family="Bovine Consensus Sequence (BCS)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="lysozyme"
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/protein_id="AAC37311.1"
/db_xref="GI:16332"
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NWLCLTKWESSYNTKATNYNPSSESTDYGIFGINSKWWCNDGKTPNAVDGCHVSCSEL
MENDIAKAYACAKHIVSEQGITAWVAWKSHCRDHDVSSYVEGCTL"
                                                                                                                                                             /gene="lysozyme"
                                                                                                                                                                                                              /note="putative"
/rpt_family="Nla"
                                                                                                                                                                                                                                                                                                             /gene="lysozyme"
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=exon1
join(2537. .2672,3840. .4004,6136. .6211,7575. .7641)
/gene="lysozyme"
                                                                                                                                          'note="putative"
                                                                                                                                                                                                                                              'gene="lysozyme"
                                                                                                                                                                                                                                                                                                 rpt_family="BCS"
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/db_xref="taxon:9913"
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. .8130
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     1909 g
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BOVLYSOZMC
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MEDLINE
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3960 GCANANCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCG 4004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 GCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGTGTAATGATG
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1 (bases 1 to 8051)

Irwin,D.M., White,R.T. and Wilson,A.C.

Characterization of the cow stomach lysozyme genes: repetitive DNA and concerted evolution

J. Mol. Evol. 37 (4), 355-366 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8308905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOVLYSOZMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lysozyme; repetitive DNA.
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                                                                                                                     3645.
                                                                                                                                                                                                                     /translation="MKALIIIGFLFLSVAVQGKVFERCELARTLKKLGLDGYKGYSLA
NWLCLTKWESSYNTKATNYNPSSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
MENDIAKAVACAKHIVSEQGITAWVAWKSHCRDHDVSSYVQGCTL"
                                                                                                                                                     /gene="lysozyme"
/product="lysozyme"
/note="putative"
                                                                                                                                                                                                                                                                   /product="lysozyme"
/protein_id="AAC37312.1"
/db_xref="GI:163334"
/product="lysozyme"
                 'gene="lysozyme"
                                                               /note="putative"
/rpt_family="Bovine Concensus Sequence (BCS)"
                                                                                                  /gene="lysozyme"
                                                                                                                                                                                                                                                                                                                                           /gene="lysozyme"
                                                                                                                                                                                                                                                                                                                                                       join(769. .904,2158. .2322,4118. .4193,7192. .7258)
                                                                                                                                                                                                                                                                                                                                                                                                        /gene="lysozyme"
/note="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                             716. .904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="lysozyme"
join(716. .904,2158. .2322,4118. .4193,7192. .7755)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                       /label=exon1
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                                                                                                                                     label=exon2
                                                                                                                                                                                                                                                                                                                                                                                            'number=
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                                               _type=dispersed
                                    .4193
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SHPLZM1B
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TITLE
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Best Local Similarity
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 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M32493.1 GI
lysozyme lb.
                                                                                                                                                                                                                                                                                                              1 (bases 1 to 881)
Irwin, D.M. and Wilson, A.C.
Concerted evolution of ruminant stomach lysozymes.
of lysozyme cDNA clones from sheep and deer
J. Biol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sheep abomasum, cDNA to mRNA. Ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHPLZM1B 881 bp
Sheep lysozyme 1b (lzm1b) mRNA,
M32493 J05279
                                                                                                                                                                                                                                                   Draft entry and computer-readable by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Caprinae; Ovis.
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                                             /protein_id="AAA31558.1" |
/db_xref="GI:165966" |
/translation="KVFERCELARTLKELGILDGYKGVSLANWLCLTKWESSYNTKATN
YNRGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELMENNIAKAVACAKHIVSE
QGITAWVAWKSHCRDHDVSSYVEGCSL"
/product="lysozyme 1b"
1. .17
                                                                                                                                                                               /organism="Ovis aries"
/db_xref="taxon:9940"
                                                                                                                                                 /note="lysozyme 1b precursor"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:165965
                                                                                                                                     /codon_start=
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/note="putative"
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2. .7755
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ORGANISM
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SHPLZM1C
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                SHPLZM2A
                               RESULT 14
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VERSION
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                                                                                                           160 AGCAGTTATAACACAAAAGCTACAAACTACAATCCT 195
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                                                                                                                                           46 GGACTGGACGGCTATAAGGGAGTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAA 105
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Sheep lysozyme 1c (lyz1c) mRNA,
M32494 J05279
M32494 1 GI:165967
 SHPLZM2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Concerted evolution of ruminant stomach lysozymes. of lysozyme cDNA clones from sheep and deer J. Biol. Chem. 265 (9), 4944-4952 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable sequence for [1] kindly submitted by D.M.Irwin, 01-MAR-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90202968
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1 (bases 1 to 881)
Irwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ovis aries
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                                                                              AGCAGTTATAACACAAAAGCTACAAACTACAATCCT 141
                                                                                                                                                                                                                                                                                        285
                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                        /product="lysozyme lc"
l. .17
                                                                                                                                                                                                                                                                                      /note="PCR primer"
144 c 183 g
                                                                                                                                                                                                                                                                                                                                                                   QGITAWVAWKSHCRDHDVSSYVEGCSL"
                                                                                                                                                                                                                                                                                                                                                                                /translation="KVFERCELARTLKELGLDGYKGVSLANWLCLTKWESSYNTKATNYNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSELMENNIAKAVACAKHIVSE
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145 c 182 g
                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA31559.1"
/db_xref="GI:165968"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="lysozyme lc precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Ovis aries"
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                                                                                                                                                                                                                      21.6%; Score 96; DB 4; I
100.0%; Pred. No. 1.3e-44;
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Pred. No.
                                                                                                                                                                                                                                                                                   183 g
                                                                                                                                                                                                        Mismatches
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881 bp
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1.3e-44;
mRNA
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 linear
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MAM 27-APR-1993
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LOCUS
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ORGANISM
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                                     FEATURES
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nes 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               891 bp
Bovine 15sozyme c 1sozyme 1b mRNA,
M26246 J04831 M27179
M26246.1 GI:163312
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1 (bases 1 to 881)

1 (rwin, D.M. and Wilson, A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M32495.1 GI:165969
Lysozyme Za.
Sheep abomasum, cDNA to mRNA.
Ovis aries
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                                                             Draft entry and computer-readable sequence by D.M.Irwin, 23-JUN-1989.
                                                                                                                                                                    89291894
                                                                                                                                                                                                                                                                 Multiple cDNA sequences and the evolution of
                                                                                                                                                                                                                                                                                                1 (bases 1 to 891)
Irwin,D.M. and Wilson,A.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine abomasum, cDNA to mRNA, clones lambda-cBL[3,4,35]. Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lysozyme
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                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                  lysozyme
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                                                                                                                                                                                                . Chem. 264 (19), 11387-11393 (1989)
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Location/Qualifiers
1. .891
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/protein_id="AAA31560.1"
/protein_id="AAA31560.1"
/db_xref="GI:165970"
/translation="KVFERCELARTILKELGLDGYKGVSLANWI.CLTKWESSYNTKATN
YNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSALMENDIEKAVACAKHIVSE
QGITAWVAWKSHCRDHDVSSYVEGCTL"
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144 c 183 g
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/db_xref="taxon:9940"
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                                                                                                   for [1] kindly submitted
                                                                                                                                                                                                                                                                     bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1] kindly submitted
                                                                                                                                                                                                                                                                                                                                                                                                    Pecora; Bovoidea;
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Job time
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Best Local :
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: 1382 secs
                                                                74 AGCTTGCCAGAACTCTGAAGAAACTTGGACTGGA 107
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                                                                                                                                            14 TTATTCTGGGGTTTCTCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGAGATGTG 73
                                                                                                                                                                                                             Similarity
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hilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                         /note="lysozyme 1b signal peptide"
62. 448
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                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA30627.1"
/db_xref="GI:163313"
/translation="MKAIIIIGFLFISVAVQGKVFERCELARTLKKLGLDGYKGVSLA
NWLCLTKWESSYNTKATNYNPGSESTDYGIFQINSKWWCNDGKTPNAVDGCHVSCSEL
                                                                                                                                                                                                                                                                        /product="lysozyme lb" 152 c 196 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="lysozyme 1b precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=
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                2003, 07:02:34
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Minimum DB seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
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SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:

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5554.929 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	_					
Human macrophage-e	AAD17740	22	444	6.8	30	9
Sequence of human	AAN92054	10	435	6.8	30	8
Sequence encoding	AAN70944	œ	390	6.8	30	7
Bovine lysozyme c	AAQ39092	14	964	75.9	337	σ
ss sequence of cDN	AAN92057	10	964	98.4	437	₅
Bovine Lysozyme c2	AAV08922	20	964	98.9	439	4
p1044-BoLys plasmi	AAD39129	24	10130	100.0	444	ω
Sequence encoding	AAQ05054	11	459	100.0	444	Ń
Bovine lysozyme DN	AAD39128	24	444	100.0	444	_
Description	ID	DB	Match Length DB	Match	Score	No.
				Operv		Result
	SUMMARIES					

Human breast cance	AAL19009	22	559	3.8	17	45	o
Drosophila melanog	ABL22715	23	498	3.8	17	44	
Human toetal cDNA,	AAH94220	22	438	3.8	17	43	C
Human pheromone re	AAX05828	20	338	3.8	17	42	a
Colon adenocarcino	ABL62119	24	295	3.8	17	41	a
Human cadherin-lik	AAS18958	24	40267	4.1	18	40	
Human neuroblastom	AAI96554	22	782	4.1	18	39	O
DNA encoding novel	AAS84866	23	762	4.1	18	38	
Human immune/haema	AAK62628	22	570	4.1	18	37	
Human prostate exp	ABV37238	23	390	4.1	18	36	
Sequence of the PC	×	14	20	4.1	18	<u>ა</u>	
Methanococcus jann		19	1664976	4.3	19	34	
Bovine alpha lacta		24	4532	4 .ω	19	33	ი
Sequence of the co	AAQ37838	14	2044	4.3	19	32	a
Enterococcus faeca		23	1125	-	20	3	
Human immune/haema		22	730	4.5	20	30	C
Nucleotide sequenc	AAF55437	22	614	4.5	20	29	
Human lung tumour		24	233		22	28	
Colon tumour relat				N	23	27	O
Partial DNA sequen		22	12061	&	30	26	
Sequence of human	AAQ03368	11	5648	6.8	30	25	
Human lung-specifi	AAD39104	24	2467		30	24	
DNA encoding novel	AAS66076	23	1798	6.8	30	23	
Human prostate exp	ABV24794	23	1776		30	22	
DNA encoding novel	AAS65881	23	1512		30	21	
Human macrophage~e	AAD17725	22	1512		30	20	
DNA coding for the	AAN92386	10	1496		30	19	
Sequence encoding	AAQ03369	11	1494		30	18	
Human benign prost	ABK64517	24	1483		30	17	
Pancreas cancer re	ABL70110	24	748	6.8	30	16	
Human colon cancer	ABQ58989	24	706	٠	30	15	O
Human colon cancer	AAA16339	21	657	٠	30	14	
Human colon tumour	ABL38017	24	585	٠	30	13	O
Sequence encoding	AAN70949	8	490	6. 8	30	12	
Human colon tumour	ABL37496	24	481	6.8	30	11	
Sequence encoding	AAN70943	80	447	6. 8	30	10	

ALIGNMENTS

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RESULT 1
AAD39128
ID AAD3
  Bovine; viral vector; transgenic plant; lysozyme; antibacterial; Pierce's disease; PD; Xylella fastidiosa bacterium infection; anti-Xylella reagent; grapevine; gene; ds.
Pogue G,
                                                                                                                             Key
                                                                                                                                                       Bos
                                                                                                                                                                                                                              04-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                 AAD39128 standard; DNA; 444 BP.
                                                      17-OCT-2001; 2001WO-US32147
                                                                         25-APR-2002.
                                                                                         WO200233041-A2
                                                                                                                                                                                                            Bovine lysozyme DNA.
                                                                                                                                                                                                                                                AAD39128;
                  (LARG-) LARGE SCALE BIOLOGY CORP.
                                    18-OCT-2000; 2000US-240967P
                                                                                                                                                       sp.
 Velichko
                                                                                                                            Location/Qualifiers
1..444
                                                                                                           /*tag= a
/product= "Bovine lysozyme"
                                                                                                                     /*tag=
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RESULT 2
AAQ05054
ID AAQ0
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AC AAQ0
AC AAQ0
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DT 30-C
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to viral vectors and methods for producing transgenic plants that express heterologous DNA that encode a ruminant lysozyme, preferably bovine. This lysozyme protects against diseases caused by plant pathogens particularly bacterial pathogens. The method is useful for producing bovine lysozyme in host plants e.g. grapevines. Plasmid encoding a recombinant plant virus which comprises a bovine lysozyme encoding nucleic acid, is useful for producing bovine lysozyme to a plant. It is also useful for producing bovine lysozyme protein which acts as an anti-Xylella reagent for development of a recombinant source of Bollys protein for treating grapevines against Plerce's disease (PD). The method is useful for protecting grapevines against Xylella fastidiosa bacterium infection that causes pD. The present sequence is bovine lysozyme DNA.
               Sequence encoding bovine lysosyme c2
                                                 30-OCT-1990
                                                                                                               AAQ05054 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful for protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 444 BP; 128 A; 86 C; 117 G; 113
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                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                                                                             TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                              TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                            GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                               (first entry)
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                                                                                                                DNA;
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                                                                                                                ВP
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Pred. No. 1.2e-222;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 459 BP; 132 A; 89 C; 119 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 10; Table 2; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel DNA fragments comprising Pishia pastoris GAPDH gene it's 5'-regulatory region and 3'-transcription termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAPDH; Glyceraldehyde-3-phosphate dehydrogenase;
additive homogenous recombination; bovine lysosyme
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            TACGTTGAGGGTTGCACCCTGTAA 444
                                                             CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                          GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                             GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
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                                                                                                GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                              ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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TACGTTGAGGGTTGCACCCTGTAA
                                                CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                                                                                                                                  ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                   ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
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Pred. No. 1.2e-222;
; Mismatches 0;
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RESULT 3
AAD39129
ID AAD3
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AC AAD3

AAD39129

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Bos sp.
Chimeric - Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine; viral vector; transgenic plant; lysozyme; antibacterial; Pierce's disease; PD; Xylella fastidiosa bacterium infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing bovine lysozyme (BoLys) in plants e.g. grapevines, useful fo protecting grapevines against Pierce's disease by infecting host plant with recombinant virus containing nucleic acid encoding BoLys -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-479667/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pl044-BoLys plasmid DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2000; 2000US-240967P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2001; 2001WO-US32147.
                                                                                                                                                                                                                                                                                                                           Sequence 10130 BP; 2854 A; 2078 C; 2492 G; 2706 T;
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                             5767
5947
                                                              5887
                                                                                                                              5827
                                181
                                                                                              121
                                                                                                                                                                                                                                                           444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Fig 2; 36pp; English.
                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARGE SCALE BIOLOGY CORP
               ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTTCAGATCAACAGCAAA
                                                                               GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                              TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                               TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                             ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCTTCTGTCGCTGTCCAAGGCAAGGTC
ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 6006
                                                              GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
                                                                                                                                                                                                                           Velichko S;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 5767..6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "Bovine lysozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                        Score 444; DB 24;
Pred. No. 1.2e-222;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circular; gene; ds
                                                                                                                                                                                                                                                                                         Length 10130;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                240
                                                                5946
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RESULT 4
AAV08922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΩÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
12-JAN-1995;
19-SEP-1991;
25-NOV-1991;
22-APR-1997;
                 This sequence encodes the bovine lysozyme c2 and can be used in the transgenic plant of the invention. The transgenic plant is resistant to plant pathogens and contains heterologous DNA encoding a ruminant or ruminant-like lysozyme, the plant expresses sufficient levels of the lysozyme to render it less susceptible to the pathogens than the wild-type plant. The plants are resistant to bacterial pathogens such as Pseudomonas syringae or Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                        Transgenic plants resistant to bacterial ruminant lysozyme gene
                                                                                                                                                                                                                                                                                                                                                                                       Bos sp.
                                                                                                                                                                                                                                                                                                                                                                                                           pa thogen
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine Lysozyme c2 protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV08922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV08922 standard;
                                                                                                                                                         P-PSDB;
                                                                                                                                                                   WPI; 1999-069855/06
                                                                                                                                                                                        Fitzmaurice LC,
                                                                                                                                                                                                                                                                                  22-APR-1997;
                                                                                                                                                                                                                                                                                                       15-DEC-1998
                                                                                                                                                                                                                                                                                                                           US5850025-A
                                                                                                                                                                                                                                                                                                                                                                                                                      Lysozyme; signal peptide;
                                                                                                     Example 1; Column 37-40;
                                                                                                                                                                                                           (SIBI-) SIBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6187 TACGTTGAGGGTTGCACCCTGTAA 6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                          AAW73502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                             resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                            NEUROSCIENCES
                                                                                                                                                                                                                               91US-0762679.
91US-0798223.
97US-0919093.
                                                                                                                                                                                                                                                              95US-0373390
                                                                                                                                                                                                                                                                                  97us-0919093
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
25..462
/*tag= a
                                                                                                                                                                                        Mirkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                              ds.
                                                                                                    23pp;
                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant;
                                                                                                                                                                                                             INC
                                                                                                      English.
                                                                                                                                     pathogens -
                                                                                                                                                                                                                                                                                                                                                                                                                       plant pathogen;
                                                                                                                                    contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
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Matches 439; Best Local Similarity

Conservative

0

Query Match

98.9%; 100.0%;

Score 439; Pred. No.

4.9e-220; DB 20;

Length 964; Indels

0;

Gaps

0;

Sequence 964 BP; 297

A; 165 C; 201 G; 301 T;

0 other;

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RESULT 5
AAN92057
ID AAN9
AX AAN9
AX AAN9
AX AAN9
AX BOV1
XX B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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       (SALK ) SALK
                                          02-NOV-1987;
                                                                                                               18-MAY-1989
                                                                                                                                                W08904320-A
                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ss sequence
lysozyme C2
                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine lysozyme C2; protein signal sequence; Pinchia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN92057 standard; DNA; 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGGGTTGCACCCTGTAA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACACAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of cDNA insert of clone lambda BL3 encoding together with 3' untranslated region.
     INST FOR BIOL STUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                        87US-0115940.
                                                                          88WO-U503907
                                                                                                                                                                                              /*tag= c
463..964
                                                                                                                                                                                                                /*tag= c
68..462
/*tag= d
                                                                                                                                                                                                                                                                   /standard_name=
25..462
                                                                                                                                                                                                                                                                                                                      /standard_name=
942..964
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                    "EcoRI Adaptor
                                                                                                                                                                                                                                                                                                                                       "EcoRI Adaptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pastoris
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RESULT 6
AAQ39092
ID AAQ3
XX AAQ3
AC AAQ3
XC AAQ3
XX BOV1
XX BOV1
XX BOV1
XX Gram
KW Gram
KW Toma
KW Agrc
XX Agrc
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                                                                                                                                                                                                                                                                                                    Б
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
              Bovine; lysozyme c; transgenic; plant; resistance; pathogen; gram negative; bacteria; hen egg white lysozyme; potato; tobacc tomato; carrot; apple; sunflower; petunia; violet; Pseudomonas; Agrobacterium; Xanthomonas; Erwinia; Clavibacter; ss.
                                                                                                      Bovine lysozyme c DNA.
                                                                                                                                          20-JUL-1993
                                                                                                                                                                                                              AAQ39092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1989-165613/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Digan ME, I
Williams ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                      386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harpold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                     (first entry)
                                                                                                                                                                                                            DNA;
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The 3'-noncoding sequence does not contain a polyadenylation signal or a poly (A)+ tail. The 5'-terminus does not contain the ATG triplet corresponding to the translation initiation codon fo the pre-lysozyme C2 mRNA. Thus the cDNA insert encodes 16 amino acids amino-terminal to the amino-terminus of the mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodn. of animal lysozyme - consists of P. pastoris for transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 964 BP; 298 A; 165 C; 200 G; 301 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pages 26-29; ; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                         128 TGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACT 187
                                                                                                                                                                                                                                                                                                                                                                                                                          86 GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC
                                                                                                                                                                                                         CTCTCGTTATTCTGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGAGA
AGGGTTGCACCCTGTAA
                  AGGGTTGCACCCTGTAA 444
                                                                 ACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGT
                                                                                                      TTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGTTACGTTG 427
                                                                                                                                                                                                                                                                                  ACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAATGGTGGT
                                                                                                                                                                                                                                                                                                                                                       TGGCAAACTGGTTGTGTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAGCC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.4%; Score 437;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C from pichia pastoris by secretion promoter and terminator DNA
462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thill GP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5e-219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 greater stability. The lysozyme may be applied directly to treat or protect plants such as potatoes, tobacco, tomatos, carrots, apples, sunflowers, petunias and violets from plant pathogens such as Pseudomonas, Agrobacterium, Xanthomonas, Erwinia and Clavibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence encodes bovine lysozyme c. This sequence was used in the production of transgenic plants that lare resistant to pathogens. The lysozyme encoded by this sequence has a greater ability to lyse gram negative bacteria than hen egg white lysozyme and also has a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection of plants against plant pathogens - by transformawith DNA encoding a ruminant or ruminantilike lysozyme, esp. bovine lysozyme C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAR34010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1993-117142/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-SEP-1991;
25-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 73-74; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMAR-) SMART PLANTS INT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGCGAGTCAG
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                                                                                                                                                                                                  AATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAGCAAGG 365
                                                                                                                                                                                                                                                                                                     GTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGGCAAACTGGTTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCTACAAA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGAGTCAG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTCTCGTTATTCTGGGGTTTCTCTTCCTTTCTGTCGCTGTCCAAGGCAAGGTCTTTGA
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                          TGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                           GTGTAATGATGGCAAAACCCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGCGAATT
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91US-0798223
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25..459
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mirkov TE;
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99.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 337; DB 14;
Pred. No. 1.5e-166;
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AAN70944
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A cDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHI 14-1; pHI21 and pHI 23 (contg. an approx. 500 bp insert) and pHL8 (contg. a 300 bp insert).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid plasmids contg. sequences for human lysozyme - \circ e.g. as antiviral and antibacterial agent, and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1987-136923/20
P-PSDB; AAP70596.
                                               Plasmid pHLZ100; human placental pre-lysozyme C; human milk lysozyme; human histiocytic lymphoma cell line U-937 pre-lysozyme C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; p2; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sledziewski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1985;
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                                                                                                                      Sequence of human pre-lysozyme C of placental origin.
                                                                                                                                                                             07-APR-1990
                                                                                                                                                                                                                            AAN92054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 390 BP; 113
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                                                                                                                                                                                                                                                                           AAN92054 standard; DNA; 435
                                                                                                                                                                                                                                                                                                                                                                                                       150 AAGCACTGATTATGGGATATTTCAGATCAA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                 204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; 5c.
100.0%; Pr
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Best Local Similarity
                                             Alzheimer's disease; Parkinson's disease; Huntington's disease; fibrosis; amyotrophic lateral sclerosis; lymphoid cell disorder; platelet disorder; thromborytopenia; osteoarthritis; bone degenerative disorder; thrombosis; periodontal disease; osteoporosis; tissue repair; burn; inclsion; ulcer; lung; liver; severe combined immunodeficiency; SCID; autoimune disorder; multiple sclerosis; rheumatoid arthritis; allergy; asthma; thrombolysis; coagulation disorder; hereditary disorder; haemophilia; neuroprotective; antibacterial; immunosuppressive, analgesic; vulnerary; immunostimulant;
                                                                                                                                                                                                                                                                                                             Human; macrophage-expressed protein; inflammation; angiogenesis; cancer; transplantation; myelodysplastic syndrome; transgenic animal; ischaemia; gene therapy; Crohn's disease; immune disorder; myeloid leukaemia; shock; sepsis; nephritis; genetic disorder; nervous system disease; neuropathy; sepsis; nephritis; genetic disorder; nervous system disease; neuropathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence contained in plasmid pHLZ100. Apart from the four N-terminal amino acids, it encodes the entire sequence of human pre-lysozyme C of placental origin in addition to a translational stop signal. The mature lysozyme C corresponding to the pre-lysozyme C encoded by AAN92054 has the same AA sequence as human milk lysozyme. AN92054 differs from the nucleotide sequence of the cDNAs encoding human pre-lysozyme C isolated from human histlocytic lymphoma cell line U-937 (see FT tags a and b). However, these nucleic acid differences do not alter the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodn. of animal lysozyme - consists of P. pastoris for transcription
                          vaccine; vasotropic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human macrophage-expressed cDNA #17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _Harpold MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0115940
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/*tag= a
replace(39, "A")
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C from pichia pastoris by secretion promoter and terminator DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                             haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.6e-05;
                             osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Siegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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CC of bio-pharmaceuticals, development of bio-sensors and transplantation.

CC The protein is used to manipulate stem cells in culture to give rise to comeuroepithelial cells that is used to augment or replace cells damaged comeuroepithelial cells that is used to augment or replace cells damaged comeuroepithelial cells and regeneration of nerve and brain tissue complaints are complainted to augment or central nerves and brain tissue compared to the treatment of central and peripheral nerveus system compared to the treatment of central and peripheral nerveus system compared to the treatment of central and peripheral nerveus system compared to the treatment of central and involved in compared to the compared to
                                                                                      severe combined immunodeficiency (SCID), bacterial or fungal infections autoimmune disorders eg. multiple sclerosis, rheumatoid arthritis, allergies such as asthma or other respiratory problems and is involved in thrombolysis or thrombosis is useful in treatment of coagulation disorders (hereditary disorders such as haemophilia) or to enhance coagulation and other haemostatic events in treating wounds resulting from trauma, surgery and inhibits the growth, effects blorhythms or
                   metabolism, catabolism, anabolism, processing utilisation, storage elimination of dietary fat, lipid, protein, carbohydrate, vitamins
                                                                      circadian cycles of rhythms, fertility of male or female subjects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rewarmia and myelodysplastic syndromes. The protein exhibits activity relating to angiogenesis, cytokine, stem cell growth factor activity and activity/inhibin related activities and is involved in proliferation, differentiation and survival of pluripotent and totipotent stem cells and useful for re-engineering damaged or diseased tissues, manufacture of blo-pharmaconticals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 150; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126
31-MAR-2000; 2000US-0540217
11-DEC-2000; 2000US-0255200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and its protein. The invention is used in gene therapy and in creating transgenic animals. Macrophage-expressed molecule is useful treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel macrophage-expressed nucleic acids and polypeptides for diagnosis and treatment of inflammatory, autoimmune, neurological, myeloid or lymphoid cell disorders, cancer and for promoting wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory conditions such as nephritis, Crohn's disease, ischaemia-
reperfusion injury, shock, sepsis, immune responses, cancer and myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dickson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE -) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200164839-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to an isolated macrophage-expressed cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
68..349
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14..67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                          storage or
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minerals, provides analgesic effects or other pain

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RESULT 10
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Best Local :
                                                                                                                                                                                                                                    A cDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and pHL2 and pHL8 (contg. a 300 bp insert).
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                                                                                                                                                                                                                                                                                                                                                                                                        New hybrid plasmids contg. sequences for human lysozyme - useful e.g. as antiviral and antibacterial agent, and transformed hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sledziewski A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE3540075-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; antiviral; bacteriolytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin like activity and as an antigen in a vaccine composition to raise an immune response. The present sequence is human macrophage-
                                                                                                                                                                                                     Sequence 447 BP; 122 A; 81 C; 125 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Claim 5; p2; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1987-136923/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1985;
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ilarity 100.0%;
Conservative
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                                                                                                                                                                Length 447;
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Best Local (
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Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -
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20-FEB-2001; 2001US-270216P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; colon cancer; colon tumour antigen; cytostatic; vaccine; colon tumour metastatic antigen; diagnosis; gene; ss.
Claim 1; SEQ ID 1085; 105pp; English.
                                                                                                                                                                 WPI; 2002-114514/15.
                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon tumour antigen polynucleotide SEQ ID NO:1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL37496 standard; cDNA; 481
                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                       Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                2001WO-US18557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                       Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour. Sequence 481 BP; 127 A; 93 C; 128 G; 131 T; 2 other; 6.8%; Score 30; Pred. No. DB 24; 1.6e-05; Length 481;

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204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                               30;
                                       Similarity
                              ilarity 100.0%;
Conservative 0;
                               Mismatches
                                Indels
                                0,
                                Gaps
                                0
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AAGCACTGATTATGGGATATTTCAGATCAA 218

AAN70949; AAN70949 standard; cDNA; 490 BP.

Sequence encoding human lypozyme (HLZ) on cDNA clone HL14-1.

(first entry)

Antibacterial; antiviral; bacteriolytic; phagocytosis; ss

Homo sapiens

Location/Qualifiers 19..454

RESULT 11

0,

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RESULT 13
ABL38017/c
ID ABL380
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Best Local
     Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them useful for inhibiting development of cancer in patient -
                                                                                                                                   09-JUN-2000; 2000US-210899P.
20-FEB-2001; 2001US-270216P.
                                                           WPI; 2002-114514/15.
                                                                                                            (CORI-) CORIXA CORP
                                                                                                                                                                         08-JUN-2001; 2001WO-US18557
                                                                                                                                                                                                  20-DEC-2001.
                                                                                                                                                                                                                           WO200196388-A2
                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                   Human; colon cancer; colon tumour antigen; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                            Human colon tumour antigen polynucleotide SEQ ID NO:1606
                                                                                                                                                                                                                                                                                                                                         08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                  ABL38017;
                                                                                                                                                                                                                                                                                                                                                                                       ABL38017 standard; cDNA; 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A CDNA bank was constructed using total RNA isolated from the human lymphoma cell line U-937. The bank was tested by hybridising with two radio-labeled 17-mer oligonucleotides (equiv. to the AA sequences 26-31 and 63-68 of HLZ). Clones isolated were designated pHL 14-1; pHL21 and pHL 23 (contg. an approx. 500 bp insert) and pHL8 (contg. a 300 bp insert).
                                                                                                                                                                                                                                                                         colon tumour metastatic antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 490 BP; 122 A; 100 C; 149 G; 119 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 4; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hybrid plasmids contg. sequences for human lysozyme - ue.g. as antiviral and antibacterial agent, and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid plasmids contg. sequences for human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AAGCACTGATTATGGGATATTTCAGATCAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                    Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85DE-3540075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.8%;
                                                                                  Secrist H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 490;
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HANGE CON CONTRACT OF THE CONT
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                          This sequence represents a human nucleotide sequence which is differentially expressed in colon cancer cells compared to the expression levels in normal cells. The nucleotide sequence can be used as a source of primers and probes. The nucleotide sequence is useful for determining the phenotype of a cell by detecting the differential expression of the sequence relative to a normal cell. The probes derived from the sequence can also be used to determine the phenotype of cells in a sample. Probes and antibodies which hybridise to the nucleotide sequence can also be used to determine the phenotype of cells in a sample for detecting a mutation in a test nucleotide sequence and also for detecting cancer, preferably colon cancer. Antibodies against the protein encoded by the nucleotide sequence can also be used in a method to detect colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endege WO,
Catino TJ,
Schlegel R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 263; 345pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and proteins for identifying therapeutic agents useful for treating and diagnosing cancer, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-256641/22.
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27-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 1606; 105pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AAGCACTGATTATGGGATATTTCAGATCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; detect; differential expression; human; mutation; non-invasive diagnostic method; ds.
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diagnostic method is non-invasive and accurate
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Pred. No.
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Lewis ME, Molino GA, Mona
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for diagnosing

colon cancer at an early stage.

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ARESULT 15
ARQ5899/c
ID ABQ589
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                                                                                                                                                                                                                                                                                       ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially cexpressed in cancer tissues. ABB78993 to ABB79004 represent proteins cencoded by the ABQ60786 to ABQ60787 nucleic acid sequences. (I) can be used in antisense therapy. An antibody immunoreactive with a polypeptide concoded by (I) is useful for detecting cancer in a patient sample, and concoded by (I) is useful for detecting cancer in a patient sample, and concoded by a presence or absence of a polypucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived concoded to the presence of a nucleic acid which concoded concoded to the presence of a nucleic acid which concoded concoded to the presence of a nucleic acid which concoded concoded to the presence of a nucleic acid which concoded to the presence of t
                                                                                                                 Query Match
Best Local Similarity
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Best Local :
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     puryess C, Astle JH, Carroll E, Thiaglingam A, Lewis ME;
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                                                                                                                                                                                                                                   Sequence 706 BP; 196 A; 156 C; 134 G; 206 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 796pp; English.
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Search completed: July Job time : 182 secs 5, 2003, 06:20:13

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES	
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444		- 1	13	BG937925	BG937925 1Abo09H04
444	100.0	462	ш Ш	BG938107	BG938107 1Abo11D05
444	100.0	463	13	BG938377	BG938377 1Abo16E03
444	100.0	464	13	BG938413	BG938413 1Abo07G10
444	100.0	469	13	BG938112	
444	100.0	476	13	BG937589	BG937589 1Abo03C3

Result No.

Score

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ALIGNMENTS

	JOURNAL COMMENT	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	RESULT 1 BG937925 LOCUS DEFINITION ACCESSION
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada Tel: 780 492 0169 Fax: 780 492 4265 Email: smoore@afns.ualberta.ca The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 898.0 and E-value of 0.0 PCR PRIMER'S FORWARD: M13 Forward BACKWARD: M13 Reverse	Unpublished (2001) Contact: Dr. Stephen Moore . Beef Genomics Laboratory Dept of AFMS, University of Alberta	Bovidae; Bovinae; Bos. 1 (bases 1 to 453) Moore,S.S., Hansen,C., Li,C., Fu,A., Meng,Y. and Li,G. CDNA's from bovine abomasum tissue	벌	BG937925 1Abo09H04 Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA sequence. BG937925 BG937925 BG937925

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KEYWORDS
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 Contact: Dr.
             Unpublished
                                       Moore, S.S.,
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/leb_host="XLI-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
87 c 121 g 116 t
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Seq primer: T3 primer
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 916.0 and E-value of 0.0
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                                                                                                                                                                          CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                                                                                                                                       GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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                                                                                                                                              CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
                                                                                       TACGTTGAGGGTTGCACCCTGTAA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Eplihellal"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
/clome_lib="Boyine Abomasum cDNA Library"
/sex="Two males and one female mixed"
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Pred. No. 1.5e-223;
               463 bp
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cDNA 5',
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ACCESSION VERSION

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                                                                                                                                                                                                                                                           200
                                                                                                                                                                                                                                                                            181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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421 TACGTTGAGGGTTGCACCCTGTAA 444
                                                                      361 CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT 420
                                                                                                                                              301 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
1 (bases 1 to 463)
Moore, S.S., Hansen, C., Li, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTTCCTGTCGCCTGTCCAAGGCAAGGTC 60
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos
) in main database at high score of 918.0 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: M13 Forward BACKWARD: M13 Reverse
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                                                                                                                                                                                                                                                                                                                                                    GTCAGCCTGGCAAACTGGTTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
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                                                                                                          ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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                                    CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
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/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
91 c 119 g 120 t
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/db_xref="taxon:9913"
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Pred. No. 1.5e-223;
); Mismatches 0;
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Moore, S.S., Hansen, C., Li, C., Fu, A.,
cDNA's from botine abomasum tissue
Unpublished (2001)
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smoore@afns.ualberta.ca
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            TGGTGGTGTAATGATGCCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC 300
                                                                                      ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                                                                       GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAAACACAAAAGCT 193
                                                                                                                                                                                                              TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 133
TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                     ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho_I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Pred. No. 1.5e-223;
Mismatches 0;
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                                 61
                                                              17
                                                          BACKWARD: M13 Reverse
Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: M13 Forward BACKWARD: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 930.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                                                                 POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moore, S.S., Hansen, C., Li, C., Fu, A CDNA's from bovine abomasum tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COW
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                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG938112.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                                                                    133
                                                                                                                          Conservative
                                                                                                                                                                                            /note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
92 c 123 g 121 t
                                                                                                                                                                                                                                          /tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithellal"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
                                                                                                                                                                                                                                                                                                               /organism-"Bos taurus"
/db_xref="taxon:9913"
/clone_lib-"Bovine Abomasum cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                         /sex="Two males and one female mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                     100.0%; Score 444; DB 13; 100.0%; Pred. No. 1.5e-223;
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                                                                                                                         Mismatches
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CDNA 5', mRNA
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GTCAGCCTGGCAAACTGGTTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                                                                                                                           BACKWARD: M13 Reverse
Seq primer: T3 primer
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moore,S.S., Hansen,C., Li,C., Fu,A.,
CDNA's from bovine abomasum tissue
Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                               The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 944.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                   Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                               FORWARD: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                    Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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Bovine Abomasum cDNA
                                                            /clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'.strain"
            /note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
94 c 122 g 125 t
                                                                                                                                                                       /organism="Bos taurus"
/db_xref="taxon:9913"
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High quality sequence stop: 476
                                                                                                                                     The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme) in main database at high score of 944.0 and E-value of 0.0
                                                                                                                                                                            Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                  Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                      Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                                                               cDNA's from bovine abomasum tissue
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                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                              POLYA-NO
                                                                                                 BACKWARD: M13 Reverse
                                                                                                                FORWARD: M13 Forward
                                                                                                                             PCR PRimers
                                                                                                                                                             Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGATCAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGTTGAGGGTTGCACCCTGTAA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAGGCTCTCGTTATTCTGGGGTTTCTTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                                                                                                                                                                             Beef Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGGCATTACAGCCTGGGTGGCATGGAAAAGTCATTGTCGAGACCATGACGTCAGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 476)
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 Bovine Abomasum cDNA Library Bos
                                                                                                                                                                                                                                                                                                                                                                                 GI:14337575
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                                                                                                                                                                                                                                                                                                                                                                                                                             476 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                     Edmonton,
  cDNA Library"
                                                                                                                                                                                                                                                                            Meng, Y.
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BG937601
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Best Local :
                                                                                                              JOURNAL
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                                                                                                                                                                                                                                    sequence.
BG937601
BG937601.1
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                                                                                                            CDNA's from bovine abomasum Unpublished (2001)
                                                                                                                                     Moore, S.S.,
                                                                                                                                                                                                  Bos taurus
                                                                                                                                                                                                                COW
                                                                                                                                                                                                                                                                           1Abo03H1 Bovine
                                                                                                                                                                                                                                                                                       BG937601
                                                                                                                                                               Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                (bases 1 to 478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135
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                                                                                                                                                               Bos.
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241 TGGTGGTGAATGATGGCAAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 TGGTGGTGTAATGATGGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTCAGCCTGGCAAACTGGTTTGTGTTTTGACCAAATGGGAAAGCAGTTATAAACACAAAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCTTCTGTCGCTGTCCAAGGCAAGGTC
                                                                          Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)in main database at high score of 948.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRE'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
I; Site_2: Xho I"
1; Site_2: Xho I"
23 g 125 t
                                                                                                                                                                                                                                                                              Hansen, C., Li, C., Fu, A.,
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Pred. No. 1.5e-223;
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                                                                                                                              Edmonton,
                                                                                                                                                                                                                                                                              Meng,Y.
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AUTHORS
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                                                                                                                                                                       DEFINITION
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                              Bovidae; Bovinae; Bos.
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                            Bos taurus
                                                                                          COW.
                                                                                                          EST
                                                                                                                       BG937832.1
                                                                                                                                       sequence.
BG937832
                                                                                                                                                                     1Abo07G03
                                                                                                                                                                                    BG937832
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Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR PRimers
FORWARD: M13 Forward
Moore,S.S.,
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                                                                                                                                                                                                                                                                                             TACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                                                                                                                                                                                                                                                                                   GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGGTGTAATGACGCAAAACCCCTAATGCAGTTGACGGCTGTCATGTATCCTGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCAGCCTGGCAAACTGGTTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAAGGCTCTCGTTATTCTGGGGGTTTCTCTTTCCTTTCTGTCGCTGTCCAAGGCAAGGTC
              (bases 1 to 481)
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/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
15 c 123 g 125 t
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Bovine Abomasum cDNA Library Bos taurus cDNA 5', mRNA
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/db_xref="taxon:9913"
/clone_11b="Bovine Abomasum cDNA Library"
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Hansen, C., Li, C.,
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Pred. No. 1.5e-223;
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
BG937936 4
1Abo08E01 Bovine Abomasum
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Seq primer: T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)
in main database at high score of 954.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA's from bovine abomasum Unpublished (2001)
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/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
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/cell_type="Epithelial"
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Contact: Dr. Stephen Moore
Beef Genomics Laboratory
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Bos taurus
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme ')
) in main database at high score of 955.0 and E-value of 0.0
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quality sequence stop: 482
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/note="Organ: Abomasum; Vector: Uni-2ZAPXR;
I; Site_2: Xho_I"
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/cell_type="Epithelial" |
/dev_stage="Young adult" |
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/db_xref-"taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/sex="Two males and one female mixed"
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                                 181 ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240
                                                                                     121 GTCAGCCTGGCAAACTGGTTGTGTTTTGACCAAATGGGAAAGCAGTTATAACACAAAAAGCT
                                                                                                                                                                                                                                                                                     444;
                                                                                                                                                          61 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAACTTGGACTGGACGGCTATAAGGGA 120
                                                                                                                                        74 TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA
                                                                                                                                                                                                              sequence.
BG937881
                                                                                                                                                                                                                                   1 ATGAAGGCTCTCGTTATTCTGGGGGTTTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC
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410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
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Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smoore@afns.ualberta.ca
The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA)
in main database at high score of 959.0 and E-value of 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae;
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA
                                                                    GTCAGCCTGGCAAACTGGTTGTGTTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT
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/lab_host="XLI-BlueMRP'-strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
97 c 123 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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1Abo13G04
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore, S.S., Hansen, C., L1, C., Fu, A cDNA's from bovine abomasum tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smoore@afns.ualberta.ca
                   TACGTTGAGGGTTGCACCCTGTAA 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dr.
                                                                                                                                                                                                       /lab_host="XL1-BlueMRF'-strain"
/note="Organ: Abomasum; Vector:
                                                                                                                                                                                                                                                        /clone_lib-"Bovine Abomasum cDNA Library"
/sex-"Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/cell_type="Epithelial"
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                                                                                                                                                                                                                                                                                                                           /organism="Bos taurus"
/db_xref="taxon:9913"
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BG937882
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Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
Tel: 780 492 0169
Fax: 780 492 4265
                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA's from bovine abomasum Unpublished (2001)
Contact: Dr. Stephen Moore
                                                                                                                                                                                                                                 FORWARD: M13 Forward BACKWARD: M13 Reverse Seq primer: T3 primer
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Moore, S.S., Hansen, C., Li, C., Fu, A.,
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                                                                                                                                                                                                     POLYA-No.
                                                                                                                                                                                                                                                                                          PCR PRimers
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) in main database at high score of 963
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                                                                                                                                                                                                                                                                                                                                    Email: smoore@afns.ualberta.ca
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                                                                                                                                                                                                                   quality sequence stop:
/dev_stage="Young adult"
/lab_host="XII-BlueMRF'-strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR
I; Site_2: Xho I"
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/tissue_type="Gastrointestinal tissue (GIT)"
                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
                                                                  /cell_type="Epithelial"
                                                                                                                                                                                  Location/Qualifiers
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Li,G

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Canada

7A mRNA

EST 11-JUN-2001 CDNA 5', mRNA

Gaps

70

ECOR

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SOURCE
ORGANISM
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BG938101
BG938101.1
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                                                                                                                                                                       Contact: Dr Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A,
                                                                                                                                                                                                                                                                                                                                                               EST
                POLYA=No.
                                          Seq primer: T3 primer
                                                         BACKWARD: M13 Reverse
                                                                   PCR PRimers
FORWARD: M13 Forward
                                                                                                   The sequence best matches gb:BOVLZYM7A (Bos) in main database at high score of 963.0 ar
                                                                                                                                Email: smoore@afns.ualberta.ca
                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
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                                                                                    AUTHORS
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1Abo14E01
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Dept of AFNS, University of Alberta 410 Agri/For, Dept of AFNS, U of A, Tel: 780 492 0169
                                       Unpublished (2001)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
                                                                                                                                                                                        COW.
                                                                                    Moore, S.S., Hansen, C., Li, C., Fu, A., cDNA's from bovine abomasum tissue
                                                                                                                                Bovidae; Bovinae;
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                         Bos taurus
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                                                                                                                                                                                                                                  sequence.
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/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF'.strain"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Sisie_2: Xho I"
96 c 123 g 130 t
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/db_xref="taxon:9913"
/clone_lib="Bovine Abomasum cDNA Library"
/clone_Trwo males and one female mixed"
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The sequence best matches gb:BOVLZYM7A (Bos taurus lysozyme 7A mRNA) in main database at high score of 965.0 and E-value of 0.0
PCR PRimers
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BACKWARD: M13 Reverse
Seq primer: T3 primer
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/lab_host="XLI-BlueMRF'.strain"
/note="Organ: Abomasum; Vector:
I; Site_2: Xho I"
97 c 124 g 129 t
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/sex="Two males and one female mixed"
/tissue_type="Gastrointestinal tissue (GIT)"
/ceil_type="Epithelial"
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/db_xref="taxon:9913"
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-09-385-982-344
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Sequence 32, Appl	Sequence 32, Appl	Sequence 342, App	Sequence 2480, Ap	Sequence 40, Appl	Sequence 1740, Ap	Sequence 296, App	Sequence 2435, Ap	Sequence 16, Appl	Sequence 5, Appli	Sequence 50, Appl	Sequence 7, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 22, Appl	Sequence 3, Appli	Sequence 3, Appli

ALIGNMENTS

RESULT 1 US-07-798-223A-1 US-07-798-223A-1 Sequence 1, Application US/07798223A Patent No. 5422108 GENERAL INFORMATION: COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WOOTDER-FECT CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/798,223A FILING DATE: 19911125 CLASSIFICATION DATA: CLASSIFICATION DATA: APPLICATION DATA: 19-SEP-1991 APPLICATION UNMBER: 07/762,679 FILING DATE: 19-SEP-1991 ATTORNEY/AGENT INFORMATION: NAME: Seidman, Stephanie L. REFERENCE/DOCKET NUMBER: 33,779 REFERENCE/DOCKET NUMBER: 31,779 REFERENCE/DOCKET NUMBER: 51984 TELECOMMUNICATION INFORMATION: TELEPAX: (619)552-1311 TELEPAX: (619)552-0995 TELEFAX: (619)552-0095 INFORMATION FOR SEQ ID NO: ZIP: 60603 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Mirkov, T. Erik APPLICANT: Fitzmaurice, Leona Claire TITLE OF INVENTION: Protection of Plants Against Pathogens NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: FEATURE: MOLECULE TYPE: CDNA SEQUENCE CHARACTERISTICS: STATE: 1 NAME/KEY: STREET: 135 SC CITY: Chicago STRANDEDNESS: TOPOLOGY: unk ADDRESSEE: LENGTH: 60603 NUCLEIC ACID Illinois E: Fitch, Even, Tabin & Flannery 135 South LaSalle Street, Suite 900 964 base pairs USA unknown double US/07/798,223A

Sequence

Query Match
Best Local Sim
Matches 439;

Similarity

98.9%; Score 439; DB 1; IA 1: IA 1: 100.0%; Pred. No. 1.5e-226; Conservative 0; Mismatches 0;

DB 1; Length 964;

Indels

0;

Gaps

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GENERAL INFORMATION:

APPLICANT: ENDEGE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II

FILE REFERENCE: CCDNA-260XX

CURRENT APPLICATION NUMBER: US/09/385,982

CURRENT FILING DATE: 1999-08-30

EARLIER APPLICATION NUMBER: 09/328,111

EARLIER FILING DATE: 1999-06-08

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 60/198,639

EARLIER APPLICATION NUMBER: 60/098,639
RESULT
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; LOCATION: (1)...(657)
; OTHER INFORMATION: n -
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SEQ ID NO 344
LENGTH: 657
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Patent No. 6262334
                                                                                                                                 Query Match
                                                                                                     Matches
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NUMBER OF SEQ ID NOS: 544
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                                                        204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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Sequence 3, Application US/08621100 Patent No. 5850000
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TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
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LOCATION:
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LENGTH: 2044 base pair
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REFERENCE/DOCKET NUMBER: F.
TELECOMMUNICATION INFORMATION:
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NAME: Sara, Charles S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BLECK, GREGORY T. APPLICANT: BREMEL, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                     2036 CAGCCTGGGTGGCATGGAA 2018
                                                                                                   371 CAGCCTGGGTGGCATGGAA 389
                                                                                                                                               19;
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                                                                                                                                                           Similarity
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                                                                                                                                               Conservative
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508) 255-2182
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100.0%; Pr
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Pred. No.
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                                                                                                                                               Mismatches
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GENERAL INFORMATION:

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APPLICANT:
APPLICANT:

BLECK, G BREMEL,

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US-08-071-601-15; Sequence 15, Application US/08071601; Patent No. 5530177
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                                                                                                                                                                  RESULT 5
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TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2044 base pairs
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                              GENERAL INFORMATION:
            APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUENCE ENCOD
TITLE OF INVENTION: ALPHA-LACTALBUMIN
NUMBER OF SEQUENCES: 20
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08 FILING DATE: 22-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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                                                                                                                                                                                                                 2036 CAGCCTGGGTGGCATGGAA 2018
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                                               DNA SEQUENCE ENCODING BOVINE
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Pred. No.
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0.91;
                               METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15,
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                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,100
FILING DATE: 22-MAR-1996
                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCEALES,
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MOLECULE TYPE:
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APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
             CLASSIFICATION: 800 PRIOR APPLICATION NUMBER:
                                                                                                                                                                    ZIP: 53202-4178
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BLECK, GREGORY T. APPLICANT: BREMEL, ROBERT D.
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CTTY: MILWAUKEE
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TELEX: 26832 ANDSTARK
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                                                                                                                                                                                       COUNTRY: USA
ZIP: 53202-4178
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FILING DATE:
                                                                                                                                                          MEDIUM TYPE: Floppy disk
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                                                                                                                             PC-DOS/MS-DOS
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100.0%; Pred. No.
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               us/08/071,601
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US-08-851-190-4
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                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO:
                                                                                                                                                       REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for I
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HUMAN TSC-22-LIKE PROTEIN NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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LENGTH: 20 base pairs
TYPE: nucleic acid
             TOPOLOGY: line
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                                          STRANDEDNESS:
                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
 LIBRARY:
                                                                                                                                        TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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TOPOLOGY: linear
                                                                            LENGTH:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
TONSNOT 01
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                              linear
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                           for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                            US/08/851,190
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RESULT 9
US-08-071-601-11
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; ORGANISM: Oryza sativa
US-09-291-922-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08071601 Patent No. 5530177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/291,922
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 60/083,044
EARLIER FILING DATE: April 24, 1998
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 638377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                       CLASSIFICATION: 800 PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BLECK, GREGORY T.
APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUIT
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 3.8%; Score 17; DB
Local Similarity 100.0%; Pred. No. 11;
hes 17; Conservative 0; Mismatches
                                     APPLICATION NUMBER:
                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                      CITY: MILWAUKEE
STATE: WI
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL STREET: 100 E. WISCONSIN AVE., SUITE 1100
                 FILING DATE:
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  COUNTRY:
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                                     US/07/744,765
                                                                                                            US/08/071,601
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US-08-621-100-11
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Patent No.
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Best Local Similarity
                            TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                  NAME: Sara, Charles S
REGIZENCE NUMBER: 30,492
REFERENCE/DOCKET NUMBER: F.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2622
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: BREMEL, ROBERT D.
TITLE OF INVENTION: DNA SEQUITITLE OF INVENTION: ALPHA-LAC
                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 800 PRIOR APPLICATION NUMBER: 1
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CORRESPONDENCE ADDRESS:
                  MOLECULE TYPE:
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 22-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/744,765 FILING DATE:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                       (608) 255-2022
(608) 255-2182
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                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA SEQUENCE ENCODING BOVINE ALPHA-LACTALBUMIN AND METHODS OF USE
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US-08-726-883-7
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US-08-419-078-7
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Best Local Similarity
                                                                                                          Sequence 7, Application US/08726883 Patent No. 5676946
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-855-0572 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CI
IMMEDIATE SOURCE:
LIBRARY: Human
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3330 HILLVIEW AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
                               APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMES, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: PALO ALTO
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STRANDEDNESS: sing
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100.0%; Pi
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00.0%; Pred. No.
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3330 HILLVIEW AVENUE

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RESULT 13
US-08-419-078-8
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                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08419078 Patent No. 5587306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HAWKINS, PHILLIP R.
APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3330 HILLVIEW AVENUE
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INFORMATION FOR SEQ ID NO: 7:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/419,078
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA, J.
REGISTRATION NUMBER: 33954
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LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 180 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APP-1995
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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CTTY: PALO ALTO
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CITY: PALO ALTO
                                                                                                                                                                                                             COUNTRY: US
ZIP: 94304
                                                                       FILING DATE:
                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/726,883 FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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Pred. No.
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US-08-726-883-8
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 Query Match
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INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/419,078
FILING DATE: 10-APR-1995
ATTORNEY/ACENT INFORMATION:
NAME: LUTHER, BARBARA J.
                                              IMMEDIATE SOURCE:
LIBRARY: Human
CLONE: 067990
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 191 base pairs
                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDLIM TYPE: Floppy disk
COMPUTER: TIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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APPLICANT: SEILHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSPHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
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LIBRARY: Human Fetal Endothelial - Stressed
CLONE: 067990
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                                                                                                             TOPOLOGY:
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FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
                                                                                                                                STRANDEDNESS:
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                                                               Human Fetal Endothelial - Stressed
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100.0%; Pred. No.
tive 0; Mismatc
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Score 16;
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33;
DB 1;
Length 191;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/419,078
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: 9F0030 US
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-855-0555
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-855-0555
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-855-0555
TELECOMEDITION: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CONA
TMMEDIATE COINGE:
Search completed: July 5, 2003, 07:05:49 Job time: 43 secs
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; LIBRARY: Inflamed Adenoid
; CLOME: 159363
US-08-419-078-12
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US-08-419-078-12
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                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                              Matches
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APPLICANT: SETLHAMER, JEFFREY J.
TITLE OF INVENTION: PHOSHOLIPASE C HOMOLOG
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC:
STREET: 3330 HILLVIEW AVENUE
CITY: PALO ALTO
STATE: CA
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ZIP: 94304
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                                                                                                                                                     ch 3.6%; Score 16; DE
1 Similarity 100.0%; Pred. No. 33
16; Conservative 0; Mismatches
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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/qcT_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/qcT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US66_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 526, App	Sequence 11, Appl	Sequence 318, App	Sequence 344, App	Sequence 8226, Ap	Sequence 8226, Ap		Sequence 1606, Ap	Sequence 1606, Ap	Sequence 1606, Ap	Sequence 791, App	Sequence 1085, Ap	Sequence 1085, Ap	Sequence 1085, Ap	Sequence 3129, Ap	Sequence 8055, Ap	Sequence 8055, Ap	Sequence 3, Appli	Sequence 1, Appli	Description

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e 1117, 158, 177, 178, 178, 178, 178, 178, 178, 17	526
Sequence 117, App Sequence 117, App Sequence 117, App Sequence 158, App Sequence 5158, App Sequence 5019, App Sequence 5019, App Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 21, App Sequence 21, Appli Sequence 41, Appli Sequence 423, Appli Sequence 4859, App Sequence 5859, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	6, App
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ALIGNMENTS

Qy 181	Qy 121 Db 121	Qy 61 Db 61	Qy 1 Db 1	Query Match Best Local Similarity Matches 444; Conser	RESULT 1 US-09-978-199-1 Sequence 1, Application Patent NO. US200201041: Patent NO. US200201041: PAPPLICANT: POGUE, GRE APPLICANT: VELICHKO, PITTLE OF INVENTION: P. FILLE APPLICATION N CURRENT APPLICATION N CURRENT FILING DATE: PRIOR APPLICATION N PRIOR APPLICATION N PRIOR APPLICATION N PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS: SOFTWARE: Patentin Ve SEQ ID NO 1 LENGTH: 444 TYPE: DNA TYPE: DNA CRGANISM: Bovine Sp. FEATURE: NAME/KEY: CDS LOCATION: (1)(441) US-09-978-199-1
ACAAACTACAATCCTAGCAGTGAAAGCACTGATTATGGGATATTTCAGATCAACAGCAAA 240	GTCAGCCTGGCAAACTGGTTGTTGTTGACCAAATGGGAAAGCAGTTATAACACAAAAGCT 180 	TTTGAGAGATGTGAGCTTGCCAGAACTCTGAAGAAACTTGGACTGGACGGCTATAAGGGA 120 	ATGAAGGCTCTCGTTATTCTGGGGTTTCTCTTCTTTCTGTCGCTGTCCAAGGCAAGGTC 60	100.0%; Score 444; DB 10; Length 444; 100.0%; Pred. No. 1.2e-232; vative 0; Mismatches 0; Indels 0; Gaps	SULT 1 :09-978-199-1 :09-978-199-1 sequence 1, Application US/09978199 Patent No. US20020104126A1 GENERAL INFORMATION: APPLICANT: POGUE, GREGORY P. APPLICANT: VELICHKO, SHARLENE TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VERAL VECTORS FILE REFERENCE: 42202 CURRENT APPLICATION NUMBER: US/09/978,199 CURRENT FILING DATE: 2001-10-17 PRIOR FILING DATE: 2000-10-18 NUMBER OF SEQ ID NOS: 3 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 1 LENGTH: 444 TYPE: DNA ORGANISM: Bovine Sp. FEATURE: NAME/KEY: CDS LOCATION: (1)(441) y-09-978-199-1
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US-09-978-199-3
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Patent No. US20020104126A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/978,199
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: 60/240,967
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: POGUE, GREGORY P.
APPLICANT: VELICHKO, SHARLENE
TITLE OF INVENTION: PRODUCTION OF BOVINE LYSOZYME BY PLANT VIRAL VECTORS
FILE REFERENCE: 42202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
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TACGTTGAGGGTTGCACCCTGTAA 444
                                                                                          GAATTAATGGAAAATGACATCGCTAAAGCTGTAGCGTGTGCAAAGCATATTGTCAGTGAG
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RESULT 4
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 8055
LENGTH: 367
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,545
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
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PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
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PRIOR TILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
DEFICE FILING DATE: 1000-05-12
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PRIOR APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n=A,T,C
NAME/KEY: unsure
LOCATION: (361)
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NAME/KEY: unsure
LOCATION: (331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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30; Conserv
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Sequence 8055, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane

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PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3
SEQ ID NO 8055
LENGTH: 367
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                          APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/200,779 PRIOR FILING DATE: 2000-04-28
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CURRENT FILING DATE: 2001-11-06
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PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/200,999 PRIOR FILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013520US
                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (361)
OTHER INFORMATION: n-A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIOR APPLICATION NUMBER: US 60/218,950 PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/223,378
                                                                                                                                                                                                     INFORMATION:
                                                                                                                                                                                                                                                                                                                                             30;
                                                       Lodes, Michael J.
Secrist, Heather
Carter, Darrick
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                Fanger, Gary R. Smith, Carole L.
                                                                                                                    Xu, Jiangchun
Indirias, Carol Yoseph
Durham, Margarita
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 30;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
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                                                                                                                                                                                                                                                                                                                         US-09-878-178-1085
                                                                                             Sequence 1085, Application US/09878178
Patent No. US30020177552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
CURRENT FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1085
LENGTH: 478
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                SEQ ID NO 1085
LENGTH: 478
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                                                         NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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; TYPE: DNA; ORGANISM: Homo sapiens US-10-046-935-1085
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SEQ ID NO 3129
LENGTH: 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.563
CURRENT FAPLICATION NUMBER: US/10/066,543
CURRENT FILING DAYE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.527C1
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                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Aijun APPLICANT: Stolk, John A.
189 AAGCACTGATTATGGGATATTTCAGATCAA 218
                                          204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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Similarity 100.0%; Pred. No.
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Secrist, Heather
                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Susan L.
                                                                                    0;
                                                                                    Mismatches
                                                                                    3.6e-06;
hes 0;
                                                                                                                             DB 9;
                                                                                                                             Length 478;
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SED ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 791
                                                             US-10-102-524-791
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                      Query Match
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    Best Local Similarity
                                                                         ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: 447, 456, 466 OTHER INFORMATION: n = A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 791, Application US/10102524 Publication No. US20030109434A1
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LENGTH: 478
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Publication No. US20030069180A1
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Best Local Similarity
Matches 30; Conserv
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APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C2
CURRENT FILING DATE: 2002-05-14
NUMBER: OF SEQ ID NOS: 2241
RUMBER OF SEQ ID NOS: 2241
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APPLICANT: Harlocker,
APPLICANT: Secrist, He
                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                  LENGTH: 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 AAGCACTGATTATGGGATATTTCAGATCAA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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100.0%; Pred. No. 3.6e-06;
vative 0; Mismatches 0;
  6.8%;
100.0%;
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  Score 30;
Pred. No.
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DB 9; L
3.6e-06;
                  Length 522;
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RESULT 12
US-10-146-502-1606/c
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US-09-878-178-1606/c
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CURRENT FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 2237
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1606
LENGTH: 582
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SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1606

LENGTH: 582

TYPE: DNA

ORGANISM: Homo sapiens
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                                                                                                                                              Matches
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                                                                                                                                                                Best
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APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527
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CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILLING DATE: 2002-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan
APPLICANT: Secrist, Heather
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                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                           Local
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                                                                         511 AAGCACTGATTATGGGATATTTCAGATCAA 482
                                                                                                         204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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                                                                                                                                                           6.8%; Score 30; DB 9; L
L00.0%; Pred. No. 3.7e-06;
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Pred. No. 3.7e-06;
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                                                                                                                                           Indels
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Sequence 1606, Application US/10146502; Publication No. US20030069180A1

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FILE DEFERENCE: 210121.527C2

CURRENT APPLICATION NUMBER: US/10/146,502

CURRENT FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2241

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 1606

LENGTH: 582

TYPE: DNA

ORGANISM: Homo sapiens

US-10-146-502-1606
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                                                                                                           RESULT 14
US-09-796-692-8226
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APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
                                                       Sequence 8226, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2544
LENGTH: 606
TYPE: DNA
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                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/060,036 CURRENT FILING DATE: 2002-01-30
                                    APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n - A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 603
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                       204 AAGCACTGATTATGGGATATTTCAGATCAA 233
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Secrist, Heather
Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang, Aijun
                      Algate, Paul A.
                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 30; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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100.0%; Pred. No.
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hes 0;
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                                                                                                                                                                                                                                                                                                                   Sequence 8226, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
             TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and They
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                              APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane APPLICANT: Retter, Marc
PRIOR APPLICATION NUMBER: US 60/200,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (603)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
LOCATION: (615)
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NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/218,950 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636
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Retter, Marc
Corixa Corporation
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100.0%; Pred. No. 3.7e-(
tive 0; Mismatches
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...URE FILING DATE: 2000-04-27

PRIOR PELICATION NUMBER: US 60/200,303
...LOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR PRIOR APPLICATION NUMBER: US 60/200,099

PRIOR PRIOR PRILING DATE: 2000-05-04

PRIOR PELICATION NUMBER: US 60/200,084

PRIOR PELICATION NUMBER: US 60/200,084

PRIOR APPLICATION NUMBER: US 60/200,081

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR PRIOR PELICATION NUMBER: US 60/202,084

PRIOR PELICATION NUMBER: US 60/202,084

PRIOR PELICATION NUMBER: US 60/202,084

PRIOR PELICATION NUMBER: US 60/223,416

PRIOR PELICATION NUMBER: US 60/223,416

PRIOR PELICATION NUMBER: US 60/223,378

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